

Please mail w/ Action 6/15/06

; LENGTH: 18
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: yes
 US-09-078-954-14

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

RESULT 14
 US-09-325-193A-51
 ; Sequence 51, Application US/09325193A
 ; Patent No. 6406705
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Heather L.
 ; APPLICANT: Schorr, Joachim
 ; APPLICANT: Krieg, Arthur M.
 ; TITLE OF INVENTION: Use of Nucleic Acids Containing
 ; FILE REFERENCE: C1039/7025/HCL
 ; CURRENT APPLICATION NUMBER: US/09/325,193A
 ; PRIOR FILING DATE: 1999-08-03
 ; PRIOR APPLICATION NUMBER: US 09/154,614
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: PCT/US98/04703
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: US 60/040,376
 ; PRIOR FILING DATE: 1997-03-10
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Oligonucleotide
 US-09-325-193A-51

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

RESULT 15
 US-09-724-426-17
 ; Sequence 17, Application US/09724426
 ; Patent No. 6414134
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John
 ; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
 ; FILE REFERENCE: 10412-024
 ; CURRENT APPLICATION NUMBER: US/09/724,426
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-724-426-17

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 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

Search completed: May 4, 2006, 07:23:50
 Job time : 39.069 secs

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RESULT 10
US-09-082-649B-58
; Sequence 58, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR FILING DATE: 1997-05-20
; PRIOR FILING DATE: 1997-05-20
; PRIOR FILING DATE: 1997-05-20
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
; OTHER INFORMATION: chimera
US-09-082-649B-58

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGTT 20
Db 1 TCCATGACGTTCTCGAGTT 20

RESULT 11
US-09-325-193A-86
; Sequence 86, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; PRIOR FILING DATE: 1999-06-03
; PRIOR FILING DATE: 1998-09-16
; PRIOR FILING DATE: 1998-09-16
; PRIOR FILING DATE: 1998-03-10
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-325-193A-86

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGTT 20
Db 1 TCCATGACGTTCTCGAGTT 20
RESULT 12
US-09-325-193A-90
; Sequence 90, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR FILING DATE: 1998-09-16
; PRIOR FILING DATE: 1998-09-16
; PRIOR FILING DATE: 1998-03-10
; PRIOR FILING DATE: 1998-03-10
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-325-193A-90

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGTT 20
Db 1 TCCATGACGTTCTCGAGTT 20

RESULT 13
US-09-191-170-97
; Sequence 97, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 1998-10-30
; PRIOR FILING DATE: 1997-10-30
; PRIOR FILING DATE: 1996-10-30
; PRIOR FILING DATE: 1995-02-07
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 42.2989 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-4

Perfect score: 20
Sequence: 1 999gtcaactgtgagggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgm2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgm2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/1/ina/6 COMB.seq.*
6: /cgm2_6/ptodata/1/ina/6 COMB.seq.*
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8: /cgm2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-08-738-652-12
2	20	100.0	20	3	US-09-030-701-63
3	20	100.0	20	3	US-08-960-774-90
4	20	100.0	20	3	US-09-082-649B-52
5	20	100.0	20	3	US-09-082-649B-59
6	20	100.0	20	3	US-09-191-170-47
7	20	100.0	20	3	US-09-337-619-12
8	20	100.0	20	3	US-09-965-101-52
9	20	100.0	20	3	US-09-965-101-59
10	20	100.0	20	3	US-09-672-126B-1
11	20	100.0	20	3	US-09-672-126B-135
12	20	100.0	21	3	US-09-672-126B-156
13	18.4	92.0	20	3	US-08-386-063-1
14	18.4	92.0	20	3	US-08-386-063-1
15	17.4	87.0	19	3	US-09-030-701-21
16	17.4	87.0	19	3	US-09-286-098-52
17	17.4	87.0	19	3	US-08-960-774-12
18	17.4	87.0	19	3	US-09-325-193A-46
19	17.4	87.0	19	3	US-09-954-987B-61
20	17.4	87.0	19	3	US-09-672-126B-68
21	16.8	84.0	20	3	US-09-786-532-2
22	16.8	84.0	20	3	US-09-672-126B-5
23	16.8	84.0	20	3	US-09-672-126B-6
24	16.8	84.0	20	3	US-09-672-126B-24

Sequence 136, App
Sequence 151, App
Sequence 17, Appl
Sequence 148, App
Sequence 15733, A
Sequence 41, Appl
Sequence 27, Appl
Sequence 78, Appl
Sequence 1222, Ap
Sequence 921, App
Sequence 921, App
Sequence 27, Appl
Sequence 27, Appl
Sequence 165, App
Sequence 2945, Ap
Sequence 18227, A
Sequence 15817, A
Sequence 4875, Ap
Sequence 18, Appl
Sequence 174326,
Sequence 174518,

ALIGNMENTS

RESULT 1
US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACCTGAGGGGGG 20
Db 1 GGGGTCAACCTGAGGGGGG 20

RESULT 2
US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; EARLIER FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405

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6/15/06

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; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; 60 kDa cysteine rich outer membrane protein from
; Chlamydia trachomatis.
US-09-303-862-12

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGACGTT 20
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DB 1 TCCATGACGTTCTCTGACGTT 20

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RESULT 3
US-08-738-652-10
; Sequence 10, Application US/08/738,652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-10

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGACGTT 20
   |||||
DB 1 TCCATGACGTTCTCTGACGTT 20

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RESULT 4
US-09-030-701-62
; Sequence 62, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; LPS-ASSOCIATED DISORDERS
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28

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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-62

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGACGTT 20
   |||||
DB 1 TCCATGACGTTCTCTGACGTT 20

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RESULT 5
US-09-286-098-100
; Sequence 100, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; Immune System Using Immunotherapeutic Oligonucleotides and
; Cytokines
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-100

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGACGTT 20
   |||||
DB 1 TCCATGACGTTCTCTGACGTT 20

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RESULT 6
US-09-286-098-105
; Sequence 105, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; Immune System Using Immunotherapeutic Oligonucleotides and
; Cytokines
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA

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CURRENT APPLICATION NUMBER: US/09/303,862
 CURRENT FILING DATE: 1999-05-03
 EARLIER APPLICATION NUMBER: 09/133,774
 EARLIER FILING DATE: 1998-08-12
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 12
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Chlamydia trachomatis
 FEATURE:
 OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
 60 kDa cysteine rich outer membrane protein from
 Chlamydia trachomatis.
 US-09-303-862-12

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3
 US-08-738-652-10
 Sequence 10, Application US/08738652B
 Patent No. 6207646
 GENERAL INFORMATION:
 APPLICANT: Krieg, Arthur M.
 TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
 FILE REFERENCE: C1039/7004 HCL
 CURRENT APPLICATION NUMBER: US/08/738,652B
 CURRENT FILING DATE: 1996-10-30
 EARLIER APPLICATION NUMBER: US 08/276,358
 EARLIER FILING DATE: 1994-07-15
 EARLIER APPLICATION NUMBER: US 08/386,063
 EARLIER FILING DATE: 1995-02-07
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide
 US-08-738-652-10

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 4
 US-09-030-701-62
 Sequence 62, Application US/09030701B
 Patent No. 6214806
 GENERAL INFORMATION:
 APPLICANT: Krieg, Arthur M.
 APPLICANT: Schwartz, David A.
 TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
 UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
 LPS-ASSOCIATED DISORDERS
 FILE REFERENCE: C1039/7011
 CURRENT APPLICATION NUMBER: US/09/030,701B
 CURRENT FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/039,405
 PRIOR FILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 65
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 62
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic oligonucleotide
 US-09-030-701-62

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
 US-09-286-098-100
 Sequence 100, Application US/09286098
 Patent No. 6218371
 GENERAL INFORMATION:
 APPLICANT: Krieg, Arthur M.
 APPLICANT: Weiner, George
 TITLE OF INVENTION: Methods and Products for Stimulating the
 Immune System Using Immunotherapeutic Oligonucleotides and
 Cytokines
 FILE REFERENCE: C1039/7026/HCL
 CURRENT APPLICATION NUMBER: US/09/286,098
 CURRENT FILING DATE: 1999-04-02
 EARLIER APPLICATION NUMBER: US 60/080,729
 EARLIER FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 100
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Sequence
 US-09-286-098-100

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 6
 US-09-286-098-105
 Sequence 105, Application US/09286098
 Patent No. 6218371
 GENERAL INFORMATION:
 APPLICANT: Krieg, Arthur M.
 APPLICANT: Weiner, George
 TITLE OF INVENTION: Methods and Products for Stimulating the
 Immune System Using Immunotherapeutic Oligonucleotides and
 Cytokines
 FILE REFERENCE: C1039/7026/HCL
 CURRENT APPLICATION NUMBER: US/09/286,098
 CURRENT FILING DATE: 1999-04-02
 EARLIER APPLICATION NUMBER: US 60/080,729
 EARLIER FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 105
 LENGTH: 20
 TYPE: DNA

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Please mail w/ Action 6/15/06

RESULT 10
US-09-082-649B-58
; Sequence 58, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
; OTHER INFORMATION: chimera
US-09-082-649B-58

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
US-09-325-193A-86
; Sequence 86, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-86

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-09-325-193A-90
; Sequence 90, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-90

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13
US-09-191-170-97
; Sequence 97, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; TITLE OF INVENTION: for Activating Dendritic Cells
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-97

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STIC-Biotech/ChemLib

188459

From: Chan, Christina
Sent: Wednesday, May 03, 2006 9:14 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: sequence search request

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, May 02, 2006 11:53 AM
To: Chan, Christina
Subject: sequence search request

Christina,
please approve, 2 month amdt. due.

STIC

10/789758

Please do a commercial and interference sequence search on SEQ ID NO: 1-7 of the above application.

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA#
AA#:
S/L:
Oligomer:
Encode/Transl:
Structure #:
Text:
Inventor:
Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 08:17:52 ; Search time 456.437 Seconds
(without alignments)
178.449 Million cell updates/sec

Title: US-10-789-758A-1

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

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- 4: /SIDSS7/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 8: /SIDSS7/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
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- 11: /SIDSS7/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
- 12: /SIDSS7/ptodata/2/pubpna/US10_NEW_PUB.seq3.*
- 13: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq1.*
- 15: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 16: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 17: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 18: /SIDSS7/ptodata/2/pubpna/US11_NEW_PUB.seq5.*
- 19: /SIDSS7/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	US-10-619-279-10
3	20	100.0	20	US-10-435-656-10
4	20	100.0	20	US-10-881-661-3
5	20	100.0	20	US-10-533-634-43
6	20	100.0	20	US-10-382-822-10
7	20	100.0	20	US-11-296-572-10
8	20	100.0	20	US-11-025-858-3
9	20	100.0	20	US-11-025-858-7
10	20	100.0	20	US-11-127-654-63
11	20	100.0	20	US-11-127-654-82
12	20	100.0	20	US-11-127-654-130
13	20	100.0	20	US-11-127-654-145
14	20	100.0	20	US-11-127-654-146

15	20	100.0	20	17	US-11-127-654-292	Sequence 232, App
16	20	100.0	20	17	US-11-127-654-916	Sequence 916, App
17	20	100.0	20	17	US-11-154-324-1	Sequence 1, Appli
18	20	100.0	20	17	US-11-089-426-22	Sequence 22, Appl
19	20	100.0	20	17	US-11-134-918-10	Sequence 10, Appl
20	20	100.0	20	17	US-11-031-460-10	Sequence 10, Appl
21	20	100.0	20	17	US-11-087-177-45	Sequence 45, Appl
22	20	100.0	20	17	US-11-114-325-1	Sequence 1, Appli
23	20	100.0	20	17	US-11-033-039-906	Sequence 906, App
24	20	100.0	20	17	US-11-067-587-10	Sequence 10, Appl
25	20	100.0	20	17	US-11-141-690-3	Sequence 3, Appli
26	20	100.0	20	17	US-11-178-316-19	Sequence 19, Appl
27	20	100.0	20	17	US-11-089-683-61	Sequence 61, Appl
28	20	100.0	20	18	US-11-081-882-1	Sequence 1, Appli
29	20	100.0	20	18	US-11-268-170-16	Sequence 16, Appl
30	20	100.0	20	11	US-10-482-112D-2	Sequence 2, Appli
31	18.4	92.0	20	17	US-11-127-654-221	Sequence 221, App
C 32	18.4	92.0	1191	10	US-10-750-185-47485	Sequence 47485, A
C 33	18.4	92.0	1191	10	US-10-750-623-47485	Sequence 47485, A
34	18	90.0	20	10	US-10-497-591A-37	Sequence 37, Appl
35	18	90.0	20	10	US-10-497-591A-38	Sequence 38, Appl
36	18	90.0	20	17	US-11-127-654-303	Sequence 303, App
37	17	85.0	17	10	US-10-619-279-70	Sequence 70, Appl
38	17	85.0	17	12	US-10-382-822-70	Sequence 66, Appl
39	17	85.0	17	17	US-11-127-654-66	Sequence 12, Appl
40	16.8	84.0	20	10	US-10-469-561-9	Sequence 9, Appli
41	16.8	84.0	20	10	US-10-619-279-7	Sequence 7, Appli
42	16.8	84.0	20	10	US-10-619-279-73	Sequence 73, Appl
43	16.8	84.0	20	10	US-10-435-656-7	Sequence 7, Appli
44	16.8	84.0	20	10	US-10-435-656-35	Sequence 35, Appl
45	16.8	84.0	20	10		

ALIGNMENTS

RESULT 1
US-10-469-561-5
; Sequence 5, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-5

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2
US-10-619-279-10
; Sequence 10, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-10

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3
US-10-435-656-10
; Sequence 10, Application US/10435656
; Publication No. US20050277604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-10

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 4
US-10-881-661-3
; Sequence 3, Application US/10881661

; Publication No. US20060002928A1
; GENERAL INFORMATION:
; APPLICANT: Radhakrishnan, Suresh
; APPLICANT: Pease, Larry R.
; APPLICANT: Iijima, Koji
; APPLICANT: Kita, Hirohito
; TITLE OF INVENTION: Methods And Molecules For Modulating An Immune Response
; FILE REFERENCE: 07039-520001
; CURRENT APPLICATION NUMBER: US/10/881,661
; CURRENT FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-881-661-3

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
US-10-533-634-43
; Sequence 43, Application US/10533634
; Publication No. US20060019239A1
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Ivins, Bruce
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF PREVENTING INFECTIONS FROM BIOTERRORISM AGENTS WITH
; FILE REFERENCE: 4239-67021-06
; CURRENT APPLICATION NUMBER: US/10/533,634
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034523
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,964
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: K oligonucleotide
US-10-533-634-43

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 6
US-10-382-822-10
; Sequence 10, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.

Qy 1 TCCATGACGTTCTCTGACGTT 20

Qy 1 TCCATGACGTTCTTGACGTT 20
|||||

Db 1 TCCATGACGTTCTTGACGTT 20
|||||

RESULT 10
US-11-127-654-63
; Sequence 63, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-63

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
US-11-127-654-82
; Sequence 82, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (8)-(8)
; OTHER INFORMATION: m5C
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (17)-(17)
; OTHER INFORMATION: m5C
US-11-127-654-82

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-11-127-654-130
; Sequence 130, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-130

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13
US-11-127-654-145
; Sequence 145, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-145

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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
553.412 Million cell updates/sec

Title: US-10-789-758A-1

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

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Searched: 9793542 seqs, 4134689005 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	20	3	US-09-768-012-3
3	20	100.0	20	3	US-09-824-468-100
4	20	100.0	20	3	US-09-824-468-105
5	20	100.0	20	3	US-09-949-194-1
6	20	100.0	20	3	US-09-917-222-1
7	20	100.0	20	3	US-09-800-266A-86
8	20	100.0	20	3	US-09-800-266A-90
9	20	100.0	20	3	US-09-895-007A-86
10	20	100.0	20	3	US-09-895-007A-90
11	20	100.0	20	3	US-09-920-313-86
12	20	100.0	20	3	US-09-920-313-90
13	20	100.0	20	3	US-09-888-326-560
14	20	100.0	20	3	US-09-888-326-561
15	20	100.0	20	3	US-09-888-326-562
16	20	100.0	20	3	US-09-888-326-563
17	20	100.0	20	3	US-09-818-918-10
18	20	100.0	20	3	US-09-931-583-47
19	20	100.0	20	3	US-09-776-479-69
20	20	100.0	20	3	US-09-776-479-137
21	20	100.0	20	3	US-09-776-479-152
22	20	100.0	20	3	US-09-776-479-153
23	20	100.0	20	3	US-09-776-479-223

24	20	100.0	20	3	US-09-776-479-302	Sequence 302, App
25	20	100.0	20	3	US-09-776-479-948	Sequence 948, App
26	20	100.0	20	3	US-09-776-479-949	Sequence 949, App
27	20	100.0	20	3	US-09-776-479-950	Sequence 950, App
28	20	100.0	20	3	US-09-776-479-951	Sequence 951, App
29	20	100.0	20	3	US-09-776-479-952	Sequence 952, App
30	20	100.0	20	3	US-09-776-479-953	Sequence 953, App
31	20	100.0	20	3	US-09-776-479-954	Sequence 954, App
32	20	100.0	20	3	US-09-776-479-955	Sequence 955, App
33	20	100.0	20	3	US-09-776-479-956	Sequence 956, App
34	20	100.0	20	3	US-09-776-479-957	Sequence 957, App
35	20	100.0	20	3	US-09-776-479-958	Sequence 958, App
36	20	100.0	20	3	US-09-776-479-1023	Sequence 1023, App
37	20	100.0	20	3	US-09-954-987B-83	Sequence 83, Appli
38	20	100.0	20	3	US-09-967-464-1	Sequence 1, Appli
39	20	100.0	20	3	US-09-984-365-42	Sequence 42, Appl
40	20	100.0	20	3	US-09-776-479-69	Sequence 69, Appl
41	20	100.0	20	3	US-09-776-479-137	Sequence 137, App
42	20	100.0	20	3	US-09-776-479-152	Sequence 152, App
43	20	100.0	20	3	US-09-776-479-153	Sequence 153, App
44	20	100.0	20	3	US-09-776-479-223	Sequence 223, App
45	20	100.0	20	3	US-09-776-479-302	Sequence 302, App

ALIGNMENTS

RESULT 1

US-09-760-506-3

; Sequence 3, Application US/09760506

; Publication No. US20010034330A1

; GENERAL INFORMATION:

; APPLICANT: Kensil, Charlotte

; TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of CpG and

; TITLE OF INVENTION: Saponin and Methods Thereof

; FILE REFERENCE: 8449-153-999

; CURRENT APPLICATION NUMBER: US/09/760,506

; CURRENT FILING DATE: 2002-01-12

; PRIOR APPLICATION NUMBER: 60/200,853

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/175,840

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/128,608

; PRIOR FILING DATE: 1999-04-08

; PRIOR APPLICATION NUMBER: 60/095,913

; PRIOR FILING DATE: 1998-08-10

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Motif

US-09-760-506-3

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2

US-09-768-012-3

; Sequence 3, Application US/09768012

; Patent No. US2001004416A1

; GENERAL INFORMATION:

; APPLICANT: Davis, Heather L.

; APPLICANT: McCluskie, Michael J.

; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for

; TITLE OF INVENTION: Inducing a Th2 Immune Response
; FILE REFERENCE: C1040/7010/HCL/MAT
; CURRENT APPLICATION NUMBER: US/09/768,012
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,461
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; NAME/KEY: modified base
; LOCATION: (8)...(8)
; OTHER INFORMATION: Cytosine is unmethylated.
; NAME/KEY: modified base
; LOCATION: (17)...(17)
; OTHER INFORMATION: Cytosine is unmethylated.
US-09-768-012-3

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3
US-09-824-468-100
; Sequence 100, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-100

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 4
US-09-824-468-105
; Sequence 105, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the

; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-105

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
US-09-949-194-1
; Sequence 1, Application US/09949194
; Patent No. US20020091097A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
; FILE REFERENCE: C1037/7021 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/949,194
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230,637
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-949-194-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 6
US-09-917-222-1
; Sequence 1, Application US/09917222
; Patent No. US20020110569A1
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: VACCINES FOR BROAD SPECTRUM PROTECTION
; TITLE OF INVENTION: AGAINST DISEASES CAUSED BY NEISSERIA MENINGITIDIS
; FILE REFERENCE: CHOR001
; CURRENT APPLICATION NUMBER: US/09/917,222
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,495
; PRIOR FILING DATE: 2000-07-27

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; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG nucleotides
US-09-917-222-1

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 7
US-09-800-266A-86
; Sequence 86, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: C1037/7017(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,214
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-86

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 8
US-09-800-266A-90
; Sequence 90, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: C1037/7017(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,214
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
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```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-90

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 9
US-09-895-007A-86
; Sequence 86, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,368
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-86

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 10
US-09-895-007A-90
; Sequence 90, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,368
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-90
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Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
US-09-920-313-86
; Sequence 86, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-86

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-09-920-313-90
; Sequence 90, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-90

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13
US-09-888-326-560
; Sequence 560, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-560

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 14
US-09-888-326-561
; Sequence 561, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 561
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-888-326-561

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 15
US-09-888-326-562

; Sequence 562, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 562
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-562

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

Search completed: May 4, 2006, 09:01:07
Job time : 298.851 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:45:02 ; Search time 1417.59 Seconds
(without alignments)
660.095 Million cell updates/sec

Title: US-10-789-758A-1

Perfect score: 20
Sequence: 1 tccatgacgttcttcgacgtt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	498	10	CL978668
C 2	20	100.0	2799	10	CL978665
C 3	18.4	92.0	372	10	CW048863
C 4	18.4	92.0	460	10	CW036410
C 5	18.4	92.0	866	9	CC709713
C 6	17.4	87.0	698	7	CN928980
C 7	17.4	87.0	1062	10	CL970339
C 8	17	85.0	562	10	CW062877
C 9	17	85.0	659	10	CW124513
C 10	17	85.0	687	10	CW372789
C 11	17	85.0	703	10	CW631458
C 12	17	85.0	782	10	CW031589
C 13	17	85.0	1088	6	CD505499
C 14	17	85.0	2805	10	CL965273
C 15	16.8	84.0	287	2	BF713668
C 16	16.8	84.0	389	10	CG260054
C 17	16.8	84.0	464	1	AA171941
C 18	16.8	84.0	497	10	CL179555
C 19	16.8	84.0	510	10	CW218453
C 20	16.8	84.0	516	2	BF156008
C 21	16.8	84.0	546	1	AW065908
C 22	16.8	84.0	557	6	CA158051

C 23	16.8	84.0	614	6	CA113844
C 24	16.8	84.0	628	10	CW444501
C 25	16.8	84.0	646	6	CA109803
C 26	16.8	84.0	663	6	CA153304
C 27	16.8	84.0	668	6	CA264770
C 28	16.8	84.0	683	6	CA182313
C 29	16.8	84.0	715	5	BU253412
C 30	16.8	84.0	729	7	CV181077
C 31	16.8	84.0	758	9	CG110844
C 32	16.8	84.0	779	8	DR806582
C 33	16.8	84.0	794	10	CG334934
C 34	16.8	84.0	797	10	CNS02N06
C 35	16.8	84.0	814	5	BU205165
C 36	16.8	84.0	821	11	CNS03G84
C 37	16.8	84.0	842	10	CG319646
C 38	16.8	84.0	864	10	CG318330
C 39	16.8	84.0	908	6	CD791886
C 40	16.8	84.0	911	10	AG891719
C 41	16.8	84.0	915	10	CG318342
C 42	16.8	84.0	958	5	BQ882047
C 43	16.8	84.0	992	11	CNS040Q4
C 44	16.8	84.0	994	11	CNS042IL
C 45	16.8	84.0	1460	8	DN675999

ALIGNMENTS

RESULT 1
CL978668/c

LOCUS
CL978668

DEFINITION
Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION
CL978668

VERSION
CL978668.1

KEYWORDS
GSS.

SOURCE
Oryza sativa (indica cultivar-group)

ORGANISM
Oryza sativa (indica cultivar-group)

REFERENCE
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.

TITLE
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

JOURNAL
Unpublished (2004)

COMMENT
Contact: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China

FEATURES
Location/Qualifiers

source
1..498

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 498;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20

Db 83 TCCATGACGTTCTCTGACGTT 64

CL978668 498 bp DNA linear GSS 21-SEP-2004
OsIFCC032298 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

CL978668
CL978668.1 GI:52411839
GSS.

Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 498)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn

Rice genomic sequence.
Class: exon-trapped.

Location/Qualifiers

1..498

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

Query Match 100.0%; Score 20; DB 10; Length 498;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20

Db 83 TCCATGACGTTCTCTGACGTT 64

Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 287 row: m column: 17
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 372.
Location/Qualifiers
1. 372
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"
/db_xref="taxon:4558"
/clone="10513675"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

FEATURES
source
Query Match 92.0%; Score 18.4; DB 10; Length 372;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 267 TCCATGACGTTCTCGAGCTT 248

ORIGIN
RESULT 4
CW036410/c
LOCUS
DEFINITION
CW036410
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
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Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBLISHED
COMMENT
CONTACT: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC forward
Class: methylation filtered
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"

FEATURES
source
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCGAGCTT 20
|||||
Db 2354 TCCATGACGTTCTCGAGCTT 2335

ORIGIN
RESULT 3
CW048863/c
LOCUS
DEFINITION
CW048863
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

/db_xref="taxon:4558"
 /clone="10503742"
 /clone_lib="Sorghum methylation filtered library (LibID: 104)"
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 460;
 Best Local Similarity 95.0%; Pred. No. 2.8e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGACGTTCTGACGTT 20
 |||||
 Db 291 TCATGACGTTCCGGACGTT 272

RESULT 5

CC709713 886 bp DNA linear GSS 19-JUN-2003
 LOCUS OGUBY23TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBma0404D21,
 genomic survey sequence.

ACCESSION

CC709713
 CC709713.1 GI:32114489

KEYWORDS

SOURCE

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 886)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

TITLE

Consortium for Maize Genomics

JOURNAL

Unpublished (2002)

COMMENT

Other GSSs: OGUBY23TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: methylation filtered.

FEATURES

source

Location/Qualifiers

1..886

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBma0404D21"

/clone_lib="ZM_0.7_1.5_KB"

/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 886;
 Best Local Similarity 95.0%; Pred. No. 3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGACGTTCTGACGTT 20
 |||||
 Db 31 TCATGACGTTCCGGACGTT 50

RESULT 6

CN928980 698 bp mRNA linear EST 07-JUN-2004
 LOCUS

DEFINITION

000601AEPAA006237HT (AEPAA) Pinkie expanding leaf Malus x domestica

ACCESSION

CN928980

VERSION

CN928980.1 GI:48401793

KEYWORDS

SOURCE

ORGANISM

Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 698)
 Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janesen, B.,
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
 HortResearch Apple EST Project
 Unpublished (2004)
 Contact: Gleave, A.
 Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 Email: est@hortresearch.co.nz.

FEATURES

source

Location/Qualifiers

1..698

/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="AEPAA006237"

/tissue_type="Leaf"

/dev_stage="Expanding"

/clone_lib="(AEPAA) Pinkie expanding leaf"

/note="Vector: pBK-CMV; Library sequenced by Genesis
 Research & Development"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 698;
 Best Local Similarity 94.7%; Pred. No. 9.3e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGACGTTCTGACGTT 19
 |||||
 Db 86 TCATGACGTTCTGACGTT 104

RESULT 7

CN970339/c

LOCUS

DEFINITION

OsIFCC041133 Oryza sativa Express Library Oryza sativa (indica
 cultivar-group) genomic, genomic survey sequence.

ACCESSION

CN970339

VERSION

CN970339.1 GI:52395287

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartioideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 1062)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 Unpublished (2004)
 Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488576
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 687)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154

TITLE Sorghum genome sequencing by methylation filtration
JOURNAL PLOS Biol. 3 (1), e13 (2005)
PUBLISHED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: f5b001f048 row: n column: 16
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 687.

FEATURES
source
1. .687
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="f5b001f048n16"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/notes="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
Kb fraction, ligated into HincII-digested pBSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATGACGTTCTGAC 17
|||||
Db 102 TCATGACGTTCTGAC 86

RESULT 11
CW631458/c
LOCUS CW631458 703 bp DNA linear GSS 27-OCT-2004
DEFINITION OP_Ba0057122.f OP_Ba Oryza punctata genomic clone OP_Ba0057122
5', genomic survey sequence.
ACCESSION CW631458
VERSION CW631458.1 GI:54665420
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 703)
AUTHORS SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
OMAP Project - Purdue University
Unpublished (2004)
TITLE Oryza punctata
JOURNAL Oryza punctata
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621

Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19g.
Bases 36-738 of the raw sequence (length 1024) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0057 row: L column: 22
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
1. .703
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0057L22"
/tissue_type="young leaves"
/lab_host="DH10B-Ti phage resistant"
/clone_lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATGACGTTCTGAC 17
|||||
Db 259 TCATGACGTTCTGAC 243

RESULT 12
CW031589
LOCUS CW031589 782 bp DNA linear GSS 28-OCT-2004
DEFINITION 104_260.10500896.114 30365 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 10500896, genomic survey
sequence.
ACCESSION CW031589
VERSION CW031589.1 GI:54708321
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 782)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 260 row: e column: 06
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 782.

FEATURES
source
1. .782
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"

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/clone="1050089c"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/notes="Organ: leaf; Vector: pBCK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

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ORIGIN

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Query Match      85.0%; Score 17; DB 10; Length 782;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGAC 17
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Db 330 TCCATGACGTTCTCTGAC 346

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RESULT 13

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CD505499
LOCUS      1088 bp mRNA linear EST 12-JUN-2003
DEFINITION CDA74-A09.xld-t SHGC-CDA Gasterosteus aculeatus cDNA clone
ACCESSION  CDA74-A09 5', mRNA sequence.
VERSION     CD505499.1 GI:131436068
KEYWORDS    EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1 (bases 1 to 1088)
AUTHORS     Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
            Schmutz,J. and Myers,R.M.

```

```

TITLE       Expressed sequence tags from Gasterosteus aculeatus
JOURNAL     Unpublished (2003)
COMMENT     Contact: Kingsley, DM
            HHMI and Department of Developmental Biology
            Stanford University School of Medicine
            Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
            Tel: 650 725 5954
            Fax: 650 725 7739
            Email: kingsley@cngm.stanford.edu
            Plate: 74
            High quality sequence stop: 772.

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FEATURES

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source
Location/Qualifiers
1..1088
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"
/db_xref="taxon:69293"
/clone="CDA74-A09"
/sec="mixed male and female"
/tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/notes="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI
(5' adaptor); Site 2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a 50 bp linker primer containing an oligo dr sequence
preceded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoRI cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lacZ promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."

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ORIGIN

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Query Match      85.0%; Score 17; DB 6; Length 1088;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGAC 17
    |||||
Db 308 TCCATGACGTTCTCTGAC 324

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RESULT 14

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CL965273/c
LOCUS      2805 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC012064 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION  CL965273
VERSION     CL965273.1 GI:52385237
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 2805)
AUTHORS     Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.

```

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TITLE       An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
JOURNAL     Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.

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FEATURES

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Location/Qualifiers
1..2805
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

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ORIGIN

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Query Match      85.0%; Score 17; DB 10; Length 2805;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCATGACGTTCTCTGAC 17
    |||||
Db 2372 TCCATGACGTTCTCTGAC 2356

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RESULT 15

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BF713668
LOCUS      287 bp mRNA linear EST 31-DEC-2001
DEFINITION ESTFBL223 differential display RT-PCR clones Sus scrofa cDNA clone
BL223, mRNA sequence.
ACCESSION  BF713668
VERSION     BF713668.1 GI:18002858
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 287)
AUTHORS     Ponsuksilli,S., Wimmers,K. and Schellander,K.

```

TITLE Identification of porcine liver ESTs by differential display RT-PCR
JOURNAL Unpublished (2001)
COMMENT Contact: Ponsuksili S
Institute of Animal Breeding Science
University of Bonn
Endenicher Allee 15, Bonn 53115, Germany
Seq primer: T7 SP6
High quality sequence stop: 287
POLYA=No.

FEATURES Location/Qualifiers
source
1..287
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="BL223"
/clone_lib="differential display RT-PCR clones"
/note="Organ: liver; cDNA fragments obtained from
differential display RT-PCR banding patterns were cloned
into pGEM"

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 287;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy	1	TCCATGACGTTCTGACGTT	20
Db	14	TCCATGACGTTCTGATGCT	33

Search completed: May 4, 2006, 07:17:44
Job time : 1417.59 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:22:43 ; Search time 464.368 Seconds
(without alignments)
2448.208 Million cell updates/sec

Title: US-10-789-758A-1

Perfect score: 20
Sequence: 1 tccatgacgttctctgacgtt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR078395 Sequence
2	20	100.0	20	6	AR140451 Sequence
3	20	100.0	20	6	AR146388 Sequence
4	20	100.0	20	6	AR146393 Sequence
5	20	100.0	20	6	AR154681 Sequence
6	20	100.0	20	6	BD069973 Use of nu
7	20	100.0	20	6	BD190417 Microemul
8	20	100.0	20	6	BD205610 Method of
9	20	100.0	20	6	BD205615 Method of
10	20	100.0	20	6	BD222610 Compositi
11	20	100.0	20	6	BD251265 Enhanceme
12	20	100.0	20	6	BD261152 Methods a
13	20	100.0	20	6	BD261157 Methods a
14	20	100.0	20	6	BD261307 Methods a
15	20	100.0	20	6	BD261311 Methods a
16	20	100.0	20	6	BD261560 Vaccine.
17	20	100.0	20	6	BD267913 Methods f
18	20	100.0	20	6	BD270813 Stereoisom

19	20	100.0	20	6	BD270817
20	20	100.0	20	6	CQ753470 Sequence
21	20	100.0	20	6	CQ753471 Sequence
22	20	100.0	20	6	CQ769069 Sequence
23	20	100.0	20	6	CQ774838 Sequence
24	20	100.0	20	6	CQ788113 Sequence
25	20	100.0	20	6	CQ788199 Sequence
26	20	100.0	20	6	CQ815135 Sequence
27	20	100.0	20	6	CQ829537 Sequence
28	20	100.0	20	6	CQ829540 Sequence
29	20	100.0	20	6	CQ888029 Sequence
30	20	100.0	20	6	CQ888030 Sequence
31	20	100.0	20	6	CQ888166 Sequence
32	20	100.0	20	6	CQ888167 Sequence
33	20	100.0	20	6	CQ892043 Sequence
34	20	100.0	20	6	CQ892047 Sequence
35	20	100.0	20	6	CQ977066 Sequence
36	20	100.0	20	6	CQ977067 Sequence
37	20	100.0	20	6	CQ977068 Sequence
38	20	100.0	20	6	CQ977069 Sequence
39	20	100.0	20	6	CS024254 Sequence
40	20	100.0	20	6	CS057843 Sequence
41	20	100.0	20	6	CS083013 Sequence
42	20	100.0	20	6	CS086355 Sequence
43	20	100.0	20	6	CS088751 Sequence
44	20	100.0	20	6	CS110647 Sequence
45	20	100.0	20	6	AR182879 Sequence

ALIGNMENTS

RESULT 1	AR078395	Sequence 12 from patent US 5962636.	20 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR078395	Sequence 12 from patent US 5962636.	20 bp	DNA	linear	PAT 31-AUG-2000
DEFINITION	AR078395	Sequence 12 from patent US 5962636.	20 bp	DNA	linear	PAT 31-AUG-2000
ACCESSION	AR078395	Sequence 12 from patent US 5962636.	20 bp	DNA	linear	PAT 31-AUG-2000
VERSION	AR078395.1	GI:10005141	20 bp	DNA	linear	PAT 31-AUG-2000
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Bachmaier, K., Hessel, A., John, N., Neu, N. and Penninger, J., Martin.					
TITLE	Peptides capable of modulating inflammatory heart disease					
JOURNAL	Patent: US 5962636-A 12 05-OCT-1999;					
FEATURES	Location/Qualifiers					
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	/organism="unknown"					
	/mol_type="unassigned DNA"					

ORIGIN

Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 18;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;		
Qy	1	TCCATGACGTTCTCTGACGTT 20				
Db	1	TCCATGACGTTCTCTGACGTT 20				
RESULT 2	AR140451	Sequence 10 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR140451	Sequence 10 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
DEFINITION	AR140451	Sequence 10 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
ACCESSION	AR140451	Sequence 10 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
VERSION	AR140451.1	GI:14482947	20 bp	DNA	linear	PAT 16-JUN-2001
KEYWORDS	.					
SOURCE	Unknown.					
..ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.					

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TITLE      Immunostimulatory nucleic acid molecules
JOURNAL    Patent: US 6207646-A 10 27-MAR-2001;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned DNA"
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20

RESULT 3
AR146388
LOCUS      AR146388                20 bp      DNA
DEFINITION Sequence 100 from patent US 6218371.
ACCESSION  AR146388
VERSION     AR146388.1  GI:15109577
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Krieg,A.M. and Weiner,G.
TITLE       Methods and products for stimulating the immune system using
            immunotherapeutic oligonucleotides and cytokines
JOURNAL     Patent: US 6218371-A 10 17-APR-2001;
FEATURES
  source
    1. .20
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20

RESULT 4
AR146393
LOCUS      AR146393                20 bp      DNA
DEFINITION Sequence 105 from patent US 6218371.
ACCESSION  AR146393
VERSION     AR146393.1  GI:15109582
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Krieg,A.M. and Weiner,G.
TITLE       Methods and products for stimulating the immune system using
            immunotherapeutic oligonucleotides and cytokines
JOURNAL     Patent: US 6218371-A 10 17-APR-2001;
FEATURES
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    1. .20
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCCATGACGTTCTCTGACGTT 20

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Db      1  TCCATGACGTTCTCTGACGTT 20

RESULT 5
AR154681
LOCUS      AR154681                20 bp      DNA
DEFINITION Sequence 10 from patent US 6239116.
ACCESSION  AR154681
VERSION     AR154681.1  GI:15122734
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Krieg,A.M. and Kline,J.N.
TITLE       Immunostimulatory nucleic acid molecules
            Patent: US 6239116-A 10 29-MAY-2001;
JOURNAL
FEATURES
  source
    1. .20
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20

RESULT 6
BD069973
LOCUS      BD069973                20 bp      DNA
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
            the treatment of LPS-associated disorders.
ACCESSION  BD069973
VERSION     BD069973.1  GI:22615576
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Schwartz,D.A. and Krieg,A.M.
TITLE       Use of nucleic acids containing unmethylated CPG dinucleotide in
            the treatment of LPS-associated disorders
JOURNAL     Patent: JP 2001513776-A 62 04-SEP-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT     OS Artificial Sequence
            PN JP 2001513776-A/62
            PD 04-SEP-2001
            PF 25-FEB-1998 JP 1998537810
            PR 28-FEB-1997 US 60/039405
            PI DAVID A SCHWARTZ, ARTHUR M KRIEG
            PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
            CC synthetic oligonucleotide
            FH Key Location/Qualifiers
            FT source 1. .20
            FT /organism='Artificial Sequence'.
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    1. .20
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCCATGACGTTCTCTGACGTT 20

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Db      1  TCCATGACGTTCTCTGACGTT 20
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RESULT 7
BD190417 20 bp DNA linear PAT 17-JUL-2003
LOCUS Microemulsions with Adsorbed Macromolecules and Microparticles.
DEFINITION BD190417
ACCESSION BD190417.1 GI:33000156
VERSION JP 2002537102-A/1.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,
Ott,G.S. and Ohagan,D.
TITLE Microemulsions with Adsorbed Macromolecules and Microparticles
JOURNAL Patent: JP 2002537102-A 1 05-NOV-2002;
COMMENT Chiron Corporation
PN JP 2002537102-A/1
PD 05-NOV-2002
PF 05-FEB-2000 JP 2000600618
PR 23-JUL-1999 US 60/146391,28-OCT-1999 US 60/161997, PR
26-FEB-1999 US 60/121858
PI john barackman,manmohan simph,mildred ugozoli,jina kazazu,john
donnelly.
PI gary a ott,derek ohagan
CC Oligonucleotide Location/Qualifiers.
FH Key Location/Qualifiers
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20
|||||
RESULT 9
BD205615 20 bp DNA linear PAT 17-JUL-2003
LOCUS Method of controlling hematopoiesis by using CpG oligonucleotide.
DEFINITION BD205615
ACCESSION BD205615
VERSION BD205615.1 GI:33015385
KEYWORDS JP 2002514397-A/105.
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wagner,H. and Lipford,G.
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide
JOURNAL Patent: JP 2002514397-A 105 21-MAY-2002;
COMMENT CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC
OS Artificial Sequence
PN JP 2002514397-A/105
PD 21-MAY-2002
PF 14-MAY-1999 JP 2000547969
PR 14-MAY-1998 US 60/085516,02-FEB-1999 US 09/241653 PI
HERMANN WAGNER,GRAYSON LIPFORD
PC C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00
CC Synthetic Sequence
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20
|||||
RESULT 10
BD222610 20 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions of CPG and saponin adjuvants and uses thereof.
DEFINITION BD222610
ACCESSION BD222610
VERSION BD222610.1 GI:33032380
KEYWORDS JP 2002522510-A/2.
SOURCE Quillaja saponaria
ORGANISM Quillaja saponaria
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Quillajaaceae; Quillaja.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kensil,C.A.

```

TITLE
JOURNAL
COMMENT
Compositions of CPG and saponin adjuvants and uses thereof
Patent: JP 200252510-A 2 23-JUL-2002;
AQUILA BIOPHARMACEUTICALS INC
OS Quillaja saponaria
PN JP 200252510-A/2
PD 23-JUL-2002
PF 06-AUG-1999 JP 2000564661
PR 10-AUG-1998 US 60/095913, 08-APR-1999 US 60/128608 PI
PC A61K39/39, A61K39/00, C12N15/09, C12N15/00
CC Compositions of CPG and saponin adjuvants and uses thereof FH
KEY Location/Qualifiers
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/db_xref='taxon:32244'

FEATURES
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Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
DB 1 TCCATGACGTTCTCTGACGTT 20
|||||

RESULT 11
BD251265
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JUL-2003
Enhancement of Neisseria antigen bactericidal activity using CG
motif-containing oligonucleotide.
ACCESSION
BD251265 1 GI:33061035
VERSION
JP 2002537353-A/1.
KEYWORDS
synthetic construct
SOURCE
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Grandi, G., Rappuoli, R., Giuliani, M.M. and Pizza, M.
TITLE
Enhancement of Neisseria antigen bactericidal activity using CG
motif-containing oligonucleotide
JOURNAL
Patent: JP 2002537353-A 1 05-NOV-2002;
CHIRON SPA
COMMENT
OS Artificial Sequence
PN JP 2002537353-A/1
PD 05-NOV-2002
PF 09-FEB-2000 JP 2000500685
PR 26-FEB-1999 US 60/121792
PI GUIDO GRANDI, RINO RAPPUOLI, MARZIA MONICA GIULIANI, MARIAGRAZIA
PI PIZZA
PC A61K39/095, A61K31/7088, A61K39/39, A61P31/04//C07K14/22, C12N15/
PC 09, C12N15/00
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Db
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DEFINITION
20 bp DNA linear PAT 17-JUL-2003
Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines.
BD261152
ACCESSION
BD261152 1 GI:33070922
VERSION
JP 2002510644-A/100.
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Krieg, A.M. and Weiner, G.
TITLE
Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines
JOURNAL
Patent: JP 2002510644-A 100 09-APR-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT
OS Artificial Sequence
PN JP 2002510644-A/100
PD 09-APR-2002
PF 02-APR-1999 JP 2000542030
PR 03-APR-1998 US 60/080729
PI ARTHUR M KRIEG, GEORGE WEINER
PC A61K38/00, A61K31/7088, A61K39/00, A61P15/00, A61P35/00, A61P37/04,
PC A61K37/02
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DEFINITION
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Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines.
BD261157
ACCESSION
BD261157 1 GI:33070927
VERSION
JP 2002510644-A/105.
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Krieg, A.M. and Weiner, G.
TITLE
Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines
JOURNAL
Patent: JP 2002510644-A 105 09-APR-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT
OS Artificial Sequence
PN JP 2002510644-A/105
PD 09-APR-2002
PF 02-APR-1999 JP 2000542030
PR 03-APR-1998 US 60/080729
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PC A61K37/02

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Db 1 TCCATGACGTTCTCTGACGTT 20
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LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products for inducing mucosal immunity.
ACCESSION BD261307.1 GI:33071077
VERSION JP 2002516294-A/86.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORIGIN other sequences: artificial sequences.
1 (bases 1 to 20)
REFERENCE
AUTHORS Mccluskie,M.J. and Davis,H.L.
TITLE Methods and products for inducing mucosal immunity
JOURNAL Patent: JP 2002516294-A 86 04-JUN-2002;
LOEB HEALTH RESEARCH INSTITUTE AT THE OTTAWA HOSPITAL, CORY
PHARMACEUTICALS GROUP INC
OS Artificial Sequence
PN JP 2002516294-A/86
PD 04-JUN-2002
PF 21-MAY-1999 JP 2000550515
PR 22-MAY-1998 US 60/086393
PI MICHAEL J MCCLUSKIE, HEATHER L DAVIS
PC A61K39/00,A61K9/10,A61K9/16,A61K9/50,A61K31/70,A61K39/ PC
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PC A61P31/00,A61P35/00,A61P37/00
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LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products for inducing mucosal immunity.
ACCESSION BD261311.1 GI:33071081
VERSION JP 2002516294-A/90.
KEYWORDS
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synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
REFERENCE
AUTHORS Mccluskie,M.J. and Davis,H.L.
TITLE Methods and products for inducing mucosal immunity
JOURNAL Patent: JP 2002516294-A 90 04-JUN-2002;
LOEB HEALTH RESEARCH INSTITUTE AT THE OTTAWA HOSPITAL, CORY
PHARMACEUTICALS GROUP INC
OS Artificial Sequence
PN JP 2002516294-A/90
PD 04-JUN-2002
PF 21-MAY-1999 JP 2000550515
PR 22-MAY-1998 US 60/086393
PI MICHAEL J MCCLUSKIE, HEATHER L DAVIS
PC A61K39/00,A61K9/10,A61K9/16,A61K9/50,A61K31/70,A61K39/ PC
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PC A61P31/00,A61P35/00,A61P37/00
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GenCore version 5.1.7
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(without alignments)
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Perfect score: 18
Sequence: 1 tctcccagcgtgcgcacat 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	100.0	18	6	AR052624 Sequence
3	18	100.0	18	6	AR116926 Sequence
4	18	100.0	18	6	AR140496 Sequence
5	18	100.0	18	6	AR146347 Sequence
6	18	100.0	18	6	AR146392 Sequence
7	18	100.0	18	6	AR154716 Sequence
8	18	100.0	18	6	AR167448 Sequence
9	18	100.0	18	6	BD069938 Use of nu
10	18	100.0	18	6	BD076451 Combined
11	18	100.0	18	6	BD080525 Ribonucle
12	18	100.0	18	6	BD106497 High effi
13	18	100.0	18	6	BD187532 REGULATIO
14	18	100.0	18	6	BD190420 Microemul
15	18	100.0	18	6	BD192469 Compositi
16	18	100.0	18	6	BD205569 Method of
17	18	100.0	18	6	BD205614 Method of
18	18	100.0	18	6	BD222609 Compositi

19	18	100.0	18	6	BD228692
20	18	100.0	18	6	BD247888
21	18	100.0	18	6	BD251268
22	18	100.0	18	6	BD261111
23	18	100.0	18	6	BD261156
24	18	100.0	18	6	BD261272
25	18	100.0	18	6	BD261561
26	18	100.0	18	6	BD267876
27	18	100.0	18	6	BD267916
28	18	100.0	18	6	BD270778
29	18	100.0	18	6	CQ788114 Sequence
30	18	100.0	18	6	CQ788200 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR052619 18 bp DNA
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION AR052619
VERSION AR052619.1 GI:5975983
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 17 03-NOV-1998;
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ORIGIN

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LOCUS AR052624 18 bp DNA
DEFINITION Sequence 24 from patent US 5831066.
ACCESSION AR052624
VERSION AR052624.1 GI:5975988
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reed, J.C.

linear PAT 29-SEP-1999

TITLE	Regulation of bcl-2 gene expression
JOURNAL	Patent: US 5831066-A 24 03-NOV-1998;
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LOCUS	Sequence 1 from patent US 6140051.
DEFINITION	Accession AR116926
ACCESSION	Version AR116926.1 GI:14097832
VERSION	Keywords Unknown.
KEYWORDS	Source Unknown.
SOURCE	Organism Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Brown,L.R. and Xu,C.
TITLE	Fluorescent dibenzazole derivatives and methods related thereto
JOURNAL	Patent: US 6140051-A 1 31-OCT-2000;
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LOCUS	Sequence 55 from patent US 6207646.
DEFINITION	Accession AR140496
ACCESSION	Version AR140496.1 GI:14482992
VERSION	Keywords Unknown.
KEYWORDS	Source Unknown.
SOURCE	Organism Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
TITLE	Immunostimulatory nucleic acid molecules
JOURNAL	Patent: US 6207646-A 55 27-MAR-2001;
FEATURES	Location/Qualifiers 1..18 source /organism="unknown" /mol_type="unassigned DNA"
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TITLE	Regulation of bcl-2 gene expression
JOURNAL	Patent: US 5831066-A 24 03-NOV-1998;
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LOCUS	Sequence 59 from patent US 6218371.
DEFINITION	Accession AR146347
ACCESSION	Version AR146347.1 GI:15109536
VERSION	Keywords Unknown.
KEYWORDS	Source Unknown.
SOURCE	Organism Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Krieg,A.M. and Weiner,G.
TITLE	Methods and products for stimulating the immune system using immunotherapeutic oligonucleotides and cytokines
JOURNAL	Patent: US 6218371-A 59 17-APR-2001;
FEATURES	Location/Qualifiers 1..18 source /organism="unknown" /mol_type="unassigned DNA"
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RESULT 6	
AR146392	18 bp DNA linear PAT 08-AUG-2001
LOCUS	Sequence 104 from patent US 6218371.
DEFINITION	Accession AR146392
ACCESSION	Version AR146392.1 GI:15109581
VERSION	Keywords Unknown.
KEYWORDS	Source Unknown.
SOURCE	Organism Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Krieg,A.M. and Weiner,G.
TITLE	Methods and products for stimulating the immune system using immunotherapeutic oligonucleotides and cytokines
JOURNAL	Patent: US 6218371-A 104 17-APR-2001;
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RESULT 7	
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LOCUS	Sequence 45 from patent US 6239116.
DEFINITION	Accession AR154716
ACCESSION	Version AR154716.1 GI:15122769
VERSION	Keywords Unknown.
KEYWORDS	Source Unknown.
SOURCE	Organism Unclassified.
REFERENCE	1 (bases 1 to 18)

AUTHORS Krieg,A.M. and Kline,J.N.
 TITLE Immunostimulatory nucleic acid molecules
 JOURNAL Patent: US 6239116-A 45 29-MAY-2001;
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 LOCUS Sequence 14 from patent US 6287591.
 DEFINITION ARI67448
 ACCESSION ARI67448
 VERSION ARI67448.1 GI:17903228
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 18)
 Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
 Cullis,P., Scherrer,P. and Debeyer,D.
 Charged therapeutic agents encapsulated in lipid particles
 containing four lipid components
 Patent: US 6287591-A 14 11-SEP-2001;
 JOURNAL Location/Qualifiers

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ORIGIN

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RESULT 9

BD069938 BD069938 18 bp DNA linear PAT 27-AUG-2002
 LOCUS Use of nucleic acids containing unmethylated CPG dinucleotide in
 DEFINITION the treatment of LPS-associated disorders.
 ACCESSION BD069938
 VERSION BD069938.1 GI:22615541
 KEYWORDS JP 2001513776-A/27.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE

1 (bases 1 to 18)
 Schwartz,D.A. and Krieg,A.M.
 Use of nucleic acids containing unmethylated CPG dinucleotide in
 the treatment of LPS-associated disorders
 Patent: JP 2001513776-A 27 04-SEP-2001;
 JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION

COMMENT

OS Artificial Sequence
 PN JP 2001513776-A/27
 PD 04-SEP-2001
 PF 25-FEB-1998 JP 1998537810
 PR 28-FEB-1997 US 60/039405
 PI DAVID A. SCHWARTZ,ARTHUR M KRIEG
 PC A61K49/00, C07H21/02, C07H21/04, A01N43/04

CC synthetic oligonucleotide
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RESULT 10

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 LOCUS Combined antisense library.
 DEFINITION BD076451
 ACCESSION BD076451
 VERSION BD076451.1 GI:22622054
 KEYWORDS JP 2001519170-A/45.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 18)
 Riley,T.A., Brown,B.D. and Arnold,L.J.
 Combined antisense library
 Patent: JP 2001519170-A 45 23-OCT-2001;
 JOURNAL OASIS BIOSCIENCES INC
 COMMENT OS Artificial Sequence
 PN JP 2001519170-A/45
 PD 23-OCT-2001
 PF 28-SEP-1998 JP 2000515030
 PR 02-OCT-1997 US 60/060673,18-AUG-1998 US 09/136080 PI
 TIMOTHY A RILEY,BOB D BROWN,LYLE J ARNOLD
 PC C12Q1/69, C07H21/04, C12N15/09, C12P19/34, C12N15/00 CC
 synthetic oligonucleotide

FEATURES
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
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RESULT 11

BD080525/c BD080525 18 bp RNA linear PAT 27-AUG-2002
 LOCUS Ribonucleoside-derivative and method for preparing the same.
 DEFINITION BD080525
 ACCESSION BD080525
 VERSION BD080525.1 GI:22626128
 KEYWORDS JP 2001515087-A/4.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 18)

AUTHORS Pitech,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 4 18-SEP-2001;
STEFAN PITTSCH, PATRICK A WEISS, LUZI JENNY

COMMENT OS Artificial Sequence
PN JP 2001515087-A/4
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITTSCH, PATRICK A WEISS, LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH

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/mol_type="genomic RNA"
/db_xref="taxon:32630"

FEATURES source
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ORIGIN
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RESULT 12
BD106497 18 bp DNA linear PAT 18-SEP-2002
LOCUS High efficiency encapsulation of charged therapeutic agents in lipid vesicles.
DEFINITION
ACCESSION BD106497.1 GI:23201315
VERSION JP 2002501511-A/14.
KEYWORDS Chlamydia sp.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sample,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M., Cullis,P., Scherrer,P. and Debeyer,D.S.
TITLE High efficiency encapsulation of charged therapeutic agents in lipid vesicles
JOURNAL Patent: JP 2002501511-A 14 15-JAN-2002;
COMMENT INEX PHARMACEUTICALS CORP
PN JP 2002501511-A/14
PD 15-JAN-2002
PF 14-MAY-1998 JP 1998548646
PI SEAN C SEMPLE, SANDRA K KLIMUK, TROY HARASYM, MICHAEL J HOPE, PI STEVEN M ANSELL,
PI PETER CULLIS, PETER SCHERRER, DAN SUITE DEBEYER PC A61K9/00
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FH Key Location/Qualifiers.
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
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Db 1 TCTCCAGCGTGGCCCAT 18

RESULT 13
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LOCUS REGULATION OF bcl-2 GENE EXPRESSION.
DEFINITION
ACCESSION BD187532
VERSION BD187532.1 GI:32997271
KEYWORDS JP 2003026609-A/17.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reed,J.C.
TITLE REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 17 29-JAN-2003;
JOURNAL John C REED
COMMENT OS Artificial Sequence
PN JP 2003026609-A/17
PD 29-JAN-2003
PF 19-JUN-2002 JP 2002178753
PR 20-SEP-1993 US 08/124256
PI John c reed
CC Description of Artificial Sequence: Designed DNA based on bcl-2 gene
CC 2 gene
FH Key Location/Qualifiers.
FH Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
QY 1 TCTCCAGCGTGGCCCAT 18
|||||
Db 1 TCTCCAGCGTGGCCCAT 18

RESULT 14
BD190420 18 bp DNA linear PAT 17-JUL-2003
LOCUS Microemulsions with Adsorbed Macromolecules and Microparticles.
DEFINITION
ACCESSION BD190420
VERSION BD190420.1 GI:33000159
KEYWORDS JP 2002537102-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J., Ott,G.S. and Ohagan,D.
TITLE Microemulsions with Adsorbed Macromolecules and Microparticles
JOURNAL Patent: JP 2002537102-A 4 05-NOV-2002;
COMMENT Chiron Corporation
OS Artificial Sequence
PN JP 2002537102-A/4
PD 05-NOV-2002
PF 09-FEB-2000 JP 2000600618
PR 29-JUL-1999 US 60/146391,28-OCT-1999 US 60/161997, PR 26-FEB-1999 US 60/121858
PI John Barackman,manmohan simph,mildred ugozoli,jina kazazu, john donnelly,
PI gary s ott,derek ohagan
CC Oligonucleotide Location/Qualifiers.
FH Key Location/Qualifiers
1. .18
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/mol_type="genomic DNA"

FEATURES source
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
QY 1 TCTCCAGCGTGGCCCAT 18
|||||
Db 1 TCTCCAGCGTGGCCCAT 18


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ORIGIN /db_xref=taxon:32630"

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
   |||||
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 15
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LOCUS          18 bp DNA linear PAT 17-JUL-2003
DEFINITION    Compositions and methods for the delivery of oligonucleotides via
               the alimentary canal.
ACCESSION     BD192469
VERSION       BD192469.1 GI:33002208
KEYWORDS      JP 2002510319-A/34.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 18)
AUTHORS       Teng,C.I. and Hardee,G.
TITLES        Compositions and methods for the delivery of oligonucleotides via
               the alimentary canal
JOURNAL       Patent: JP 2002510319-A 34 02-APR-2002;
COMMENT       ISIS PHARMACEUTICALS INC
               OS Artificial Sequence
               PN JP 2002510319-A/34
               PD 02-APR-2002
               PF 01-JUL-1998 JP 1999507295
               PR 01-JUL-1997 US 08/886829
               PI CHING LEOU TENG,GREG HARDEE
               PC C12Q1/68,A61K9/127,A61K48/00,C07H21/04
               CC Description of Artificial Sequence: Novel Sequence FH . Key
               Location/Qualifiers
               Location/Qualifiers
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               /mol_type="genomic DNA"
               /db_xref=taxon:32630"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
   |||||
DB 1 TCTCCAGCGTGGCCAT 18

Search completed: May 4, 2006, 03:51:58
Job time : 422.931 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:45:02 ; Search time 1275.83 Seconds
(without alignments)
660.095 Million cell updates/sec

Title: US-10-789-758A-2

Perfect score: 18

Sequence: 1 tctccacgctgcgccat 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gsa1:*

10: gb_gsa2:*

11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	720	10 AY416379	AY416379 Homo sapi
C 2	18	100.0	737	2 BG258362	BG258362 602380147
C 3	18	100.0	741	9 CC465553	CC465553 ZMMBC038
C 4	18	100.0	919	5 BQ641946	BQ641946 AGENCOURT
C 5	18	100.0	924	5 BQ422178	BQ422178 AGENCOURT
C 6	18	100.0	954	5 BQ643236	BQ643236 AGENCOURT
C 7	18	100.0	960	3 BQ059398	BQ059398 AGENCOURT
C 8	18	100.0	980	3 BQ056709	BQ056709 AGENCOURT
C 9	18	100.0	1008	3 BQ061355	BQ061355 AGENCOURT
C 10	18	100.0	1036	3 BQ061909	BQ061909 AGENCOURT
C 11	18	100.0	1051	5 BQ642891	BQ642891 AGENCOURT
C 12	18	100.0	1064	3 BQ054417	BQ054417 AGENCOURT
C 13	18	100.0	1078	3 BQ055296	BQ055296 AGENCOURT
C 14	18	100.0	1126	3 BQ055950	BQ055950 AGENCOURT
C 15	16.4	91.1	376	7 C0314459	C0314459 EK236547
C 16	16.4	91.1	387	8 H85916	H85916 YS95C07.r1
C 17	16.4	91.1	398	8 H83468	H83468 YS91B09.r1
C 18	16.4	91.1	412	1 AA402089	AA402089 ZU53f02.r
C 19	16.4	91.1	442	8 W96258	W96258 ze42b06.r1
C 20	16.4	91.1	450	3 B1371010	B1371010 RES7807.5
C 21	16.4	91.1	478	2 B1214814	B1214814 RE20943.5
C 22	16.4	91.1	491	2 B1212997	B1212997 RE18291.5

C 23	16.4	91.1	508	6 CA695333	CA695333 wlmk8.pk0
C 24	16.4	91.1	533	2 B1163707	B1163707 RE03175.5
C 25	16.4	91.1	540	3 B1356588	B1356588 RE42769.5
C 26	16.4	91.1	563	3 B1637858	B1637858 SD19973.5
C 27	16.4	91.1	577	1 A1514786	A1514786 LD46473.5
C 28	16.4	91.1	595	3 B1482233	B1482233 RE64891.5
C 29	16.4	91.1	636	1 A1512315	A1512315 LD44124.5
C 30	16.4	91.1	649	3 B1577144	B1577144 RE70787.5
C 31	16.4	91.1	659	2 BG637068	BG637068 SD14920.5
C 32	16.4	91.1	661	1 A1108632	A1108632 GH07838.5
C 33	16.4	91.1	661	3 B1485852	B1485852 RE69202.5
C 34	16.4	91.1	666	3 B1483280	B1483280 RE66152.5
C 35	16.4	91.1	687	3 B1580210	B1580210 RE74359.5
C 36	16.4	91.1	695	1 AA990787	AA990787 LD34664.5
C 37	16.4	91.1	715	5 BX094259	BX094259 BX094259
C 38	16.4	91.1	876	10 C2719721	C2719721 OC_Ba004
C 39	16.4	91.1	975	2 BG286153	BG286153 602383365
C 40	16	88.9	231	2 BG182783	BG182783 RST1660.A
C 41	16	88.9	439	1 AW070294	AW070294 xa06g11.x
C 42	16	88.9	459	1 A1005163	A1005163 oul3c07.x
C 43	16	88.9	459	7 CR747281	CR747281 CR747281
C 44	16	88.9	470	5 BX104748	BX104748 BX104748
C 45	16	88.9	509	5 BU677370	BU677370 UI-CF-DUI

ALIGNMENTS

RESULT 1	AY416379/c	AY416379	Homo sapiens BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	720 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY416379	AY416379	GSS.				
DEFINITION	AY416379.1	GI:39772339	Homo sapiens (human)				
ACCESSION	AY416379		Homo sapiens				
VERSION	AY416379.1		Homo sapiens				
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
PUBMED							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
FEATURES							
source							
gene							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							

100.0%; Score 18; DB 10; Length 720;
100.0%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCTCCAGCGTGGCCAT 18
Db 18 TCTCCAGCGTGGCCAT 1

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BG258362/c 737 bp mRNA linear EST 13-FEB-2001
LOCUS 602380147F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4511027 5',
DEFINITION mRNA sequence.
ACCESSION BG258362
VERSION BG258362.1 GI:12768277
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="NIH_MGC_92"
/clone_lib="NIH_MGC_92"
/notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
REFERENCE
Query Match 100.0%; Score 18; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
Db 406 TCTCCAGCGTGGCCAT 389

RESULT 3
CC465553/c 741 bp DNA linear GSS 04-JUN-2003
LOCUS ZMMB0387J18f ZMMB0387J18f ZMMB0387J18 5',
DEFINITION genomic survey sequence.
ACCESSION CC465553
VERSION CC465553.1 GI:31383142
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 741)
/organism="Zea mays"
/mol_type="DNA"
/db_xref="taxon:9606"
/tissue_type="genomic survey"
/lab_host="ZMMB0387J18f"
/clone_lib="ZMMB0387J18f"
/notes="GSS clone"
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AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Rouard, K., Fuks, G., Yu, Y., Wing, R. and Messing, J.
TITLE Sequencing of the maize genome at PGIR (2003b)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 425.
Location/Qualifiers
1..741
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
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/lab_host="E. coli DH10B"
/clone_lib="ZMMB0c"
/notes="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
Db 460 TCTCCAGCGTGGCCAT 443

RESULT 4
BQ641946/c 919 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8289686 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6304926
DEFINITION 5', mRNA sequence.
ACCESSION BQ641946
VERSION BQ641946.1 GI:21766118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 919)
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6304926"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2526 row: 9 column: 07
High quality sequence stop: 582.
Location/Qualifiers
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/organism="Homo sapiens"
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/tissue_type="lymphoma, cell line"
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FEATURES
source

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/note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 919;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
|||||

Db 511 TCTCCAGCGTGGCCAT 494

RESULT 5

BQ422178/c
LOCUS
DEFINITION BQ422178 924 bp mRNA linear EST 23-MAY-2002
AGENCOURT 7827267 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6014407
5', mRNA sequence.
BQ422178
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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High quality sequence stop: 524.

FEATURES

source

Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 924;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
|||||

Db 236 TCTCCAGCGTGGCCAT 219

RESULT 6

BQ643236/c
LOCUS
DEFINITION BQ643236 954 bp mRNA linear EST 15-JUL-2002
AGENCOURT 828937 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6303439
5', mRNA sequence.
BQ643236
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LCM2522 row: i column: 08
High quality sequence stop: 594.

FEATURES

source

Location/Qualifiers
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/clone="IMAGE:6303439"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 954;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
|||||

Db 511 TCTCCAGCGTGGCCAT 494

RESULT 7

BQ059398/c
LOCUS
DEFINITION BQ059398 960 bp mRNA linear EST 29-MAR-2002
AGENCOURT 7049763 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815441
5', mRNA sequence.
BQ059398
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LCM2522 row: i column: 08
High quality sequence stop: 594.

FEATURES

source

Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Lou Staudt
             CDNA Library Preparation: Rubin Laboratory
             DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
             DNA distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LCM2070 row: 1 column: 02
             High quality sequence stop: 683.
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             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_99"
             /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Size-selected >500bp for average insert size
             1.8kb. Library constructed by Ling Hong in the laboratory
             of Gerald M. Rubin (University of California, Berkeley)
             using ZAP-cDNA synthesis kit (Stratagene) and Superscript
             II RT (Life Technologies). Note: this is a NIH_MGC
             Library."
ORIGIN
Query Match      100.0%; Score 18; DB 3; Length 960;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACGCGTGGCCAT 18
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Db 511 TCTCCACGCGTGGCCAT 494

RESULT 8
BQ056709/c
LOCUS      BQ056709
DEFINITION AGENCOURT_6940428 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5809129
5', mRNA sequence.
ACCESSION BQ056709
VERSION BQ056709.1 GI:19816049
KEYWORDS EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 980)
           NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Lou Staudt
           CDNA Library Preparation: Rubin Laboratory
           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LCM2054 row: e column: 02
           High quality sequence stop: 697.
FEATURES     Location/Qualifiers
             1..980
             /organism="Homo sapiens"
             /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="IMAGE:5809129"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match      100.0%; Score 18; DB 3; Length 980;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACGCGTGGCCAT 18
    |||||
Db 511 TCTCCACGCGTGGCCAT 494

RESULT 9
BQ061355/c
LOCUS      BQ061355
DEFINITION AGENCOURT_6859552 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920789
5', mRNA sequence.
ACCESSION BQ061355
VERSION BQ061355.1 GI:19885327
KEYWORDS EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 1008)
           NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Lou Staudt
           CDNA Library Preparation: Rubin Laboratory
           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LCM2085 row: a column: 14
           High quality sequence stop: 573.
FEATURES     Location/Qualifiers
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:5920789"
             /tissue_type="lymphoma, cell line"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_99"
             /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Size-selected >500bp for average insert size
             1.8kb. Library constructed by Ling Hong in the laboratory
             of Gerald M. Rubin (University of California, Berkeley)
             using ZAP-cDNA synthesis kit (Stratagene) and Superscript
             II RT (Life Technologies). Note: this is a NIH_MGC
             Library."
ORIGIN

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Query Match      100.0%; Score 18; DB 3; Length 1008;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
    |||||
Db 511 TCTCCAGCGTGGCCAT 494

RESULT 10
BQ061909/c
LOCUS
DEFINITION BQ061909 6854719 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5921412
5', mRNA sequence.
ACCESSION BQ061909
VERSION BQ061909.1 GI:19887364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1036)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2086 row: k column: 13
High quality sequence stop: 595.
Location/Qualifiers
1..1036
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5921412"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 99"
Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

FEATURES
source
1..1036
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5921412"
/tissue_type="lymphoma, cell line"
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Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match      100.0%; Score 18; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
    |||||
Db 511 TCTCCAGCGTGGCCAT 494

RESULT 11
BQ642891/c
LOCUS
DEFINITION BQ642891 8285835 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6292709
5', mRNA sequence.
ACCESSION BQ642891
VERSION BQ642891.1 GI:21767063

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1051)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2494 row: j column: 06
High quality sequence stop: 514.
Location/Qualifiers
1..1051
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6292709"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_99"
Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 1051;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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Db 511 TCTCCAGCGTGGCCAT 494

RESULT 12
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LOCUS
DEFINITION BQ054417 6771413 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5803679
5', mRNA sequence.
ACCESSION BQ054417
VERSION BQ054417.1 GI:19813757
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1064)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

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/Clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned

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Qy 1 TCTCCCAGCGTGGCCAT 18
db 511 TCTCCCAGCGTGGCCAT 49

RESULT 15
CO314459
LOCUS
DEFINITION EK236547.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
melanogaster cDNA clone EK236547 5, mRNA sequence.
ACCESSION CO314459
VERSION
KEYWORDS
SOURCE EST. GI:49371834
ORGANISM Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 376)
AUTHORS Kopczyński, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
Peterson, E. and Swimmer, C.
TITLE Exelixis FlyTag EST Project CK01 Library
JOURNAL Unpublished (2004)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: EK.2365 row: D column: 11
High quality sequence stop: 301.
FEATURES
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1..376
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK236547"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."
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Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 132 TCGCCAGCGTGGCCAT 149
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Job time : 1280.83 secs

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GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 07:24:16 ; Search time 268.966 Seconds
(without alignments)
553.412 Million cell updates/sec

Title: US-10-789-758A-2

Perfect score: 18
Sequence: 1 tctccagcgtgcgcacat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	US-09-760-506-2
2	18	100.0	18	3	US-09-824-468-59
3	18	100.0	18	3	US-09-824-468-104
4	18	100.0	18	3	US-09-965-116A-7
5	18	100.0	18	3	US-09-965-116A-77
6	18	100.0	18	3	US-09-965-116A-98
7	18	100.0	18	3	US-09-965-116A-99
8	18	100.0	18	3	US-09-800-266A-51
9	18	100.0	18	3	US-09-895-007A-51
10	18	100.0	18	3	US-09-835-371-21
11	18	100.0	18	3	US-09-920-313-51
12	18	100.0	18	3	US-09-835-370-21
13	18	100.0	18	3	US-09-888-326-755
14	18	100.0	18	3	US-09-888-326-756
15	18	100.0	18	3	US-09-931-732-20
16	18	100.0	18	3	US-09-818-918-55
17	18	100.0	18	3	US-09-776-479-1
18	18	100.0	18	3	US-09-776-479-54
19	18	100.0	18	3	US-09-776-479-55
20	18	100.0	18	3	US-09-776-479-91
21	18	100.0	18	3	US-09-954-987B-115
22	18	100.0	18	3	US-09-895-480A-14
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Sequence 1, Appli
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Sequence 54, Appl
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Sequence 91, Appl
Sequence 6, Appli
Sequence 51, Appl
Sequence 53, Appl
Sequence 45, Appl
Sequence 9, Appli
Sequence 24, Appl
Sequence 6, Appli
Sequence 40, Appl
Sequence 2, Appli
Sequence 45, Appl
Sequence 112, App

24 18 100.0 18 3 US-09-776-479-1
25 18 100.0 18 3 US-09-776-479-54
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40 18 100.0 18 6 US-10-290-545-24
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42 18 100.0 18 6 US-10-224-523-40
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44 18 100.0 18 6 US-10-187-264A-45
45 18 100.0 18 6 US-10-265-072-112

ALIGNMENTS

RESULT 1
US-09-760-506-2
; Sequence 2, Application US/09760506
; Publication No. US20010034330A1
; GENERAL INFORMATION:
; APPLICANT: Kensil, Charlotte
; TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of CpG and
; FILE REFERENCE: 8449-153-999
; CURRENT APPLICATION NUMBER: US/09/760,506
; PRIOR FILING DATE: 2002-01-12
; PRIOR APPLICATION NUMBER: 60/200,853
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/175,840
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/128,608
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/095,913
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-09-760-506-2

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGCGCAT 18
Db 1 TCTCCAGCGTGCGCAT 18

RESULT 2
US-09-824-468-59
; Sequence 59, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the

; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and

; TITLE OF INVENTION: Cytokines

; FILE REFERENCE: C1039/7026/HCL

; CURRENT APPLICATION NUMBER: US/09/824,468

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 09/286,098

; PRIOR FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 105

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 59

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-09-824-468-59

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 3

US-09-824-468-104

; Sequence 104, Application US/09824468

; Patent No. US20020064515A1

; GENERAL INFORMATION:

; APPLICANT: Kriegl, Arthur M.

; APPLICANT: Weiner, George

; TITLE OF INVENTION: Methods and Products for Stimulating the

; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and

; TITLE OF INVENTION: Cytokines

; FILE REFERENCE: C1039/7026/HCL

; CURRENT APPLICATION NUMBER: US/09/824,468

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 09/286,098

; PRIOR FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 105

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 104

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-09-824-468-104

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 4

US-09-965-116A-7/C

; Sequence 7, Application US/09965116A

; Patent No. US20020137714A1

; GENERAL INFORMATION:

; APPLICANT: Kandimala, Ekambar R.

; APPLICANT: Zhao, Qiuyan

; APPLICANT: Yu, Dong

; APPLICANT: Agrawal, Sudhir

; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory

; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by

; TITLE OF INVENTION: Positional Chemical Changes

; FILE REFERENCE: HVZ-479CP (47508.577)

; CURRENT APPLICATION NUMBER: US/09/965,116A

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: US 09/712,898

; PRIOR FILING DATE: 2000-11-15

; PRIOR APPLICATION NUMBER: US 60/235,452

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 60/235,453

; PRIOR FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthesis of end-blocked CpG-PS modified oligodeoxynucleotide

; OTHER INFORMATION: phosphorothioate

US-09-965-116A-7

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 18 TCTCCAGCGTGGCCAT 1

RESULT 5

US-09-965-116A-77

; Sequence 77, Application US/09965116A

; Patent No. US20020137714A1

; GENERAL INFORMATION:

; APPLICANT: Kandimala, Ekambar R.

; APPLICANT: Zhao, Qiuyan

; APPLICANT: Yu, Dong

; APPLICANT: Agrawal, Sudhir

; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory

; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by

; TITLE OF INVENTION: Positional Chemical Changes

; FILE REFERENCE: HVZ-479CP (47508.577)

; CURRENT APPLICATION NUMBER: US/09/965,116A

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: US 09/712,898

; PRIOR FILING DATE: 2000-11-15

; PRIOR APPLICATION NUMBER: US 60/235,452

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 60/235,453

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 77

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate

US-09-965-116A-77

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 6

US-09-965-116A-98

; Sequence 98, Application US/09965116A

; Patent No. US20020137714A1

; GENERAL INFORMATION:

; APPLICANT: Kandimalla, Ekambar R.
 ; APPLICANT: Zhao, Qiuyan
 ; APPLICANT: Yu, Dong
 ; APPLICANT: Agrawal, Sudhir
 ; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
 ; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
 ; TITLE OF INVENTION: Positional Chemical Changes
 ; FILE REFERENCE: HYZ-479CP (47508.577)
 ; CURRENT APPLICATION NUMBER: US/09/965,116A
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: US 09/712,898
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 60/235,452
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 60/235,453
 ; PRIOR FILING DATE: 2000-09-26
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 98
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: modified oligodeoxynucleotide phosphorothioate
 US-09-965-116A-98

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18

RESULT 7
 US-09-965-116A-99
 ; Sequence 99, Application US/09965116A
 ; Patent No. US20020137714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kandimalla, Ekambar R.
 ; APPLICANT: Zhao, Qiuyan
 ; APPLICANT: Yu, Dong
 ; APPLICANT: Agrawal, Sudhir
 ; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
 ; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
 ; TITLE OF INVENTION: Positional Chemical Changes
 ; FILE REFERENCE: HYZ-479CP (47508.577)
 ; CURRENT APPLICATION NUMBER: US/09/965,116A
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: US 09/712,898
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 60/235,452
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 60/235,453
 ; PRIOR FILING DATE: 2000-09-26
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 99
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: modified oligodeoxynucleotide phosphorothioate
 ; NAME/KEY: modified_base
 ; LOCATION: 10,14
 ; OTHER INFORMATION: g at positions 10 and 14 = 7-deazaguanine
 US-09-965-116A-99

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18

RESULT 8
 US-09-800-266A-51
 ; Sequence 51, Application US/09800266A
 ; Patent No. US20020156033A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Petersen, Deanna M.
 ; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
 ; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: C1037/7017 (HCL/MAT)
 ; CURRENT APPLICATION NUMBER: US/09/800,266A
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: US 60/187,214
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Sequence
 US-09-800-266A-51

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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 DB 1 TCTCCAGCGTGGCCAT 18

RESULT 9
 US-09-895-007A-51
 ; Sequence 51, Application US/09895007A
 ; Patent No. US20020165178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schetter, Christian
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Petersen, Deanna M.
 ; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
 ; TITLE OF INVENTION: TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
 ; FILE REFERENCE: C1041/7014 (AWS)
 ; CURRENT APPLICATION NUMBER: US/09/895,007A
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 60/214,368
 ; PRIOR FILING DATE: 2000-06-28
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 US-09-895-007A-51

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18

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RESULT 10
US-09-835-371-21
; Sequence 21, Application US/09835371
; Publication No. US20020187473A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, Eugen
; APPLICANT: BREIPOHL, Gerhard
; APPLICANT: WILL, David W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1743 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,371
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: base sequence
; OTHER INFORMATION: of PNA targeting CMV
US-09-835-371-21

Query Match          100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCAGCGTGGCCAT 18
   |||||
Db 1 TCTCCCAGCGTGGCCAT 18

RESULT 11
US-09-920-313-51
; Sequence 51, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-51

Query Match          100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCAGCGTGGCCAT 18
   |||||
Db 1 TCTCCCAGCGTGGCCAT 18

RESULT 12
US-09-835-370-21
; Sequence 21, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
```

```
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of PNA derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-21

Query Match          100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCAGCGTGGCCAT 18
   |||||
Db 1 TCTCCCAGCGTGGCCAT 18

RESULT 13
US-09-888-326-755
; Sequence 755, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 755
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-755

Query Match          100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCAGCGTGGCCAT 18
   |||||
Db 1 TCTCCCAGCGTGGCCAT 18

RESULT 14
US-09-888-326-756
; Sequence 756, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
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Thu May 4 17:31:28 2006

FILE REFERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 756
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: phosphodiester backbone
US-09-888-326-756

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
Db 1 TCTCCAGCGTGGCCAT 18

RESULT 15
US-09-931-732-20
Sequence 20, Application US/09931732
Publication No. US2003004548A1
GENERAL INFORMATION:
APPLICANT: Brown, Bob D.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
FILE REFERENCE: OASIO.001C1
CURRENT APPLICATION NUMBER: US/09/931,732
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: PCT/US00/09293
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/128,377
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-20

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
Db 1 TCTCCAGCGTGGCCAT 18

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OM nucleic - nucleic search, using sw model

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Title: US-10-789-758A-2

Perfect score: 18
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Gapop 10.0 , Gapext 1.0

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Lifting first 45 summaries

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- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq1.*
- 8: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
- 11: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
- 12: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 16: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 17: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 18: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq5.*
- 19: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	10	US-10-918-638-24
2	18	100.0	18	10	US-10-658-947-14
3	18	100.0	18	10	US-10-469-561-6
4	18	100.0	18	10	US-10-619-279-45
5	18	100.0	18	10	US-10-435-656-55
6	18	100.0	18	11	US-10-994-213-7
7	18	100.0	18	11	US-10-482-441C-1
8	18	100.0	18	11	US-10-923-112A-52
9	18	100.0	18	12	US-10-382-822-45
10	18	100.0	18	13	US-10-246-300D-24
11	18	100.0	18	14	US-11-296-572-55
12	18	100.0	18	17	US-11-127-654-1
13	18	100.0	18	17	US-11-127-654-85
14	18	100.0	18	17	US-11-081-140-6

15	18	100.0	18	17	US-11-134-918-55	Sequence 55, Appl
16	18	100.0	18	17	US-11-031-460-55	Sequence 55, Appl
17	18	100.0	18	17	US-11-067-587-55	Sequence 55, Appl
18	18	100.0	18	17	US-11-099-683-131	Sequence 131, App
19	18	100.0	18	17	US-11-099-683-132	Sequence 132, App
20	18	100.0	19	11	US-10-994-213-8	Sequence 8, Appli
c 21	18	100.0	19	11	US-10-994-213-9	Sequence 9, Appli
22	18	100.0	20	17	US-11-127-654-81	Sequence 81, Appl
23	18	100.0	23	11	US-10-994-213-1	Sequence 1, Appli
c 24	18	100.0	23	11	US-10-994-213-2	Sequence 2, Appli
c 25	18	100.0	30	17	US-11-201-322-2	Sequence 2, Appli
26	18	100.0	32	11	US-10-923-112A-19	Sequence 19, Appl
c 27	18	100.0	6030	11	US-10-826-585-4	Sequence 4, Appli
c 28	18	100.0	6030	17	US-11-000-688-408	Sequence 408, App
c 29	18	100.0	218821	17	US-11-121-086-31	Sequence 31, Appl
30	16.4	91.1	18	10	US-10-619-279-72	Sequence 72, Appl
31	16.4	91.1	18	12	US-10-382-822-72	Sequence 72, Appl
32	16.4	91.1	18	17	US-11-127-654-72	Sequence 72, Appl
33	16.4	91.1	18	17	US-11-127-654-73	Sequence 73, Appl
34	16.4	91.1	18	17	US-11-127-654-393	Sequence 393, App
35	16.4	91.1	20	17	US-11-127-654-102	Sequence 102, App
36	16.4	91.1	20	17	US-11-127-654-104	Sequence 104, App
37	16.4	91.1	20	17	US-11-127-654-105	Sequence 105, App
38	16	88.9	18	10	US-10-437-591A-40	Sequence 40, Appl
39	16	88.9	18	17	US-11-099-683-133	Sequence 133, App
c 40	16	88.9	30	18	US-11-229-183-490	Sequence 490, App
41	15.4	85.6	543	7	US-09-925-065A-555070	Sequence 555070,
42	15.4	85.6	614	7	US-09-925-065A-869047	Sequence 869047,
43	15.4	85.6	1135	7	US-09-925-065A-698222	Sequence 698222,
44	15.4	85.6	2094	7	US-09-925-065A-709635	Sequence 709635,
45	15	83.3	23	18	US-11-229-183-276	Sequence 276, App

ALIGNMENTS

RESULT 1
US-10-918-638-24
; Sequence 24, Application US/10918638
; Publication No. US20050249663A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: DERIVATIVES THEREOF
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/918,638
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US/10/246,300
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-918-638-24

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACGCTGCGCCAT 18
DB 1 TCTCCACGCTGCGCCAT 18

RESULT 2
US-10-658-947-14
; Sequence 14, Application US/10658947
; Publication No. US20050255153A1

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;
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; Agents in
; Lipid Vesicles
;
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: PO Box 5068
; CITY: Dillion
; STATE: CO
; COUNTRY: US
; ZIP: 80435
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
;
; CURRENT APPLICATION DATA: US/10/658,947
; FILING DATE: 09-Sep-2003
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,480
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: <Unknown>
; TELEFAX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: other nucleic acid
;
; HYPOTHETICAL: no
; ANTI-SENSE: yes
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
;
US-10-658-947-14

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCCAT 18
Db 1 TCTCCAGCGTGGCCCAT 18

RESULT 3
US-10-469-561-6
; Sequence 6, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
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; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-6

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCCAT 18
Db 1 TCTCCAGCGTGGCCCAT 18

RESULT 4
US-10-619-279-45
; Sequence 45, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-45

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCCAT 18
Db 1 TCTCCAGCGTGGCCCAT 18

RESULT 5
US-10-435-656-55
; Sequence 55, Application US/10435656
; Publication No. US2005027604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AMS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
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; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-55

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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Db 1 TCTCCAGCGTGGCCAT 18

RESULT 6
US-10-994-213-7/c
; Sequence 7, Application US/10994213
; Publication No. US2006001991A1
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/10/994,213
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US/09/634,320
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-994-213-7

Query Match 100.0%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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Db 18 TCTCCAGCGTGGCCAT 1

RESULT 7
US-10-482-441C-1
; Sequence 1, Application US/10482441C
; Publication No. US2006004114A1
; GENERAL INFORMATION:
; APPLICANT: Nanda Sinha
; APPLICANT: William Edward Zedalis
; APPLICANT: Gregory Keith Miranda
; TITLE OF INVENTION: Activators for Oligonucleotide Synthesis
; FILE REFERENCE: 2733.2017-001
; CURRENT APPLICATION NUMBER: US/10/482,441C
; CURRENT FILING DATE: 2003-12-30
; PRIOR APPLICATION NUMBER: PCT/GB02/03029
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,717
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: short DNA sequence synthesized by modified
; OTHER INFORMATION: phosphoramidite chemistry
US-10-482-441C-1

Query Match 100.0%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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Db 1 TCTCCAGCGTGGCCAT 18

RESULT 8
US-10-923-112A-52
; Sequence 52, Application US/10923112A
; Publication No. US20060040879A1
; GENERAL INFORMATION:
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 3293
; CURRENT APPLICATION NUMBER: US/10/923,112A
; CURRENT FILING DATE: 2004-08-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ODN aldehyde
US-10-923-112A-52

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Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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Db 1 TCTCCAGCGTGGCCAT 18

RESULT 9
US-10-382-822-45
; Sequence 45, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; FILE REFERENCE: C01039.70062.US
; CURRENT APPLICATION NUMBER: US/10/382,822
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-382-822-45

Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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DB 1 TCTCCAGCGTGGCCAT 18

RESULT 10

US-10-246-300D-24
; Sequence 24, Application US/10246300D
; Publication No. US20060074034A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS AND
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/246,300D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-246-300D-24

Query Match 100.0%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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DB 1 TCTCCAGCGTGGCCAT 18

RESULT 11

US-11-296-572-55
; Sequence 55, Application US/11296572
; Publication No. US20060089326A1
; GENERAL INFORMATION:
; APPLICANT: Kline, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Kline, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/296,572
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-296-572-55

Query Match 100.0%; Score 18; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
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DB 1 TCTCCAGCGTGGCCAT 18

RESULT 12

US-11-127-654-1
; Sequence 1, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-1

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
|||||
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 13

US-11-127-654-85
; Sequence 85, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-85

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

RESULT 14

US-11-081-140-6
 ; Sequence 6, Application US/11081140
 ; Publication No. US20050261225A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stein, Cy A
 ; APPLICANT: Benimetakaya, Lynba
 ; APPLICANT: Guzzo-Pernell, Nancy
 ; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
 ; FILE REFERENCE: 0575/63293
 ; CURRENT APPLICATION NUMBER: US/11/081,140
 ; CURRENT FILING DATE: 2005-03-15
 ; PRIOR APPLICATION NUMBER: US/10/002,884
 ; PRIOR FILING DATE: 2001-11-02
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL SEQUENCE
 ; FEATURE:
 ; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
 US-11-081-140-6

Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

RESULT 15

US-11-134-918-55
 ; Sequence 55, Application US/11134918
 ; Publication No. US20050267064A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Krieg, Arthur M.
 ; APPLICANT: Kline, Joel N.
 ; APPLICANT: Klinman, Dennis
 ; APPLICANT: Steinberg, Alfred D.
 ; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
 ; FILE REFERENCE: C1039/7048 (AWS)
 ; CURRENT APPLICATION NUMBER: US/11/134,918
 ; CURRENT FILING DATE: 2005-05-23
 ; PRIOR APPLICATION NUMBER: US/09/818,918
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 08/276,358
 ; PRIOR FILING DATE: 1994-07-15
 ; PRIOR APPLICATION NUMBER: US 08/386,063
 ; PRIOR FILING DATE: 1995-02-07
 ; PRIOR APPLICATION NUMBER: US 08/738,652
 ; PRIOR FILING DATE: 1996-10-30
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 55
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 US-11-134-918-55

Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18

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OM nucleic - nucleic search, using sw model

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Title: US-10-789-758A-3

Perfect score: 22
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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- 10: gb_sts.*
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- 13: gb_vl.*
- 14: gb_hrg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	6	AX040404 Sequence
2	22	100.0	22	6	AX063577 Sequence
3	22	100.0	22	6	AX088931 Sequence
4	22	100.0	30	6	E04650 Synthetic n
5	22	100.0	30	6	AX555928 Sequence
6	22	100.0	30	6	AX774078 Sequence
7	20.4	92.7	368	1	AY858995 Mycobacte
8	20.4	92.7	375	1	AY858990 Mycobacte
9	20.4	92.7	375	1	AY858999 Mycobacte
10	20.4	92.7	375	1	AY859007 Mycobacte
11	20.4	92.7	417	1	AY859013 Mycobacte
12	18.8	85.5	29	6	E04647 Synthetic n
13	18.8	85.5	30	6	A89781 Sequence 3
14	18.8	85.5	30	6	A90868 Sequence 3
15	18.8	85.5	30	6	BD056772 Pharmaceu
16	18.8	85.5	30	6	BD261562 Vaccine.
17	18.8	85.5	30	6	CQ788115 Sequence
18	18.8	85.5	30	6	CQ788201 Sequence

19	18.8	85.5	30	6	CQ815137 Sequence
20	18.8	85.5	30	6	CQ829542 Sequence
21	18.8	85.5	30	6	CS057845 Sequence
22	18.8	85.5	30	6	CS083015 Sequence
23	18.8	85.5	30	6	CS088753 Sequence
24	18.8	85.5	30	6	CS110649 Sequence
25	18.8	85.5	30	6	E04645 Synthetic n
26	18.8	85.5	30	6	E04649 Synthetic n
27	18.8	85.5	30	6	E04651 Synthetic n
28	18.8	85.5	30	6	E04670 Synthetic n
29	18.8	85.5	30	6	E04686 Synthetic n
30	18.8	85.5	30	6	E04690 Synthetic n
31	18.8	85.5	30	6	E04695 Synthetic n
32	18.8	85.5	30	6	E04701 Synthetic n
33	18.8	85.5	30	6	AR303120 Sequence
34	18.8	85.5	30	6	AR309881 Sequence
35	18.8	85.5	30	6	AX015199 Sequence
36	18.8	85.5	30	6	AX020949 Sequence
37	18.8	85.5	30	6	AX040170 Sequence
38	18.8	85.5	30	6	AX040405 Sequence
39	18.8	85.5	30	6	AX105265 Sequence
40	18.8	85.5	30	6	AX497779 Sequence
41	18.8	85.5	30	6	AX537411 Sequence
42	18.8	85.5	30	6	AX555927 Sequence
43	18.8	85.5	30	6	AX555929 Sequence
44	18.8	85.5	30	6	AX774079 Sequence
45	18.8	85.5	45	6	E04644 Synthetic n

ALIGNMENTS

RESULT 1	AX040404	Sequence 3 from Patent WO0062802.	22 bp	DNA	linear	PAT 18-NOV-2000
LOCUS	AX040404					
DEFINITION	Sequence 3 from Patent WO0062802.					
ACCESSION	AX040404					
VERSION	AX040404.1	GI:11230216				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE 1	Deschamps, M.					
AUTHORS	Vaccine comprising rsv antigen and cpv oligonucleotide					
TITLE	Patent: WO 0062802-A 3 26-OCT-2000;					
JOURNAL	Smithkline Beecham Biologicals s.a. (BE)					
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	/organism="synthetic construct"					
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Best Local Similarity	100.0%;	Pred. No. 32;							
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Db	1	ACCGATAACGTTGCCGGTGACG	22						
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LOCUS	AX063577			22 bp	DNA	linear	PAT 24-JAN-2001		
DEFINITION	Sequence 3 from Patent WO0100231.								
ACCESSION	AX063577								
VERSION	AX063577.1	GI:12541301							
KEYWORDS	.								
SOURCE	synthetic construct								
ORGANISM	synthetic construct								

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other sequences; artificial sequences.
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REFERENCE
AUTHORS Cohen,J., Garcon,N. and Voss,G.
TITLE Vaccines
JOURNAL Patent: WO 0100231-A 3 04-JAN-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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source Location/Qualifiers
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/note="oligonucleotide"
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Best Local Similarity 100.0%; Pred. No. 32;
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Db 1 ACCGATAACGTTGCCGGTGACG 22
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AX088931
LOCUS Garcon,N. and Voss,G.
DEFINITION Sequence 3 from Patent WO0100232.
ACCESSION AX088931
VERSION AX088931.1 GI:13397689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Garcon,N. and Voss,G.
TITLE Vaccine
JOURNAL Patent: WO 0100232-A 3 04-JAN-2001;
SMITHKLINE BEECHAM BIOLOGICS SA (BE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CpG containing oligonucleotide"
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Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
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Db 1 ACCGATAACGTTGCCGGTGACG 22
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RESULT 4
E04650
LOCUS Synthetic nucleotide with(GACGTC) structure, having immunomodulation
DEFINITION activities.
ACCESSION E04650
VERSION E04650.1 GI:2172846
KEYWORDS JP 1992352724-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 30)
Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O.,
Makino,T. and Shimada,S.
TITLE IMMUNOMODULATION TYPE THERAPEUTIC AGENT
JOURNAL Patent: JP 1992352724-A 7 07-DEC-1992;
MITSUI TOATSU CHEM INC
COMMENT OS Artificial gene
other sequences; artificial sequences.
1
REFERENCE
AUTHORS YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
TITLE TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO
ETSURO.
JOURNAL JP 1992352724-A/7
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
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Db 1 ACCGATAACGTTGCCGGTGACG 22
|||||
RESULT 5
AX555928
LOCUS Sequence 5 from Patent WO234887.
DEFINITION AX555928
ACCESSION AX555928
VERSION AX555928.1 GI:25899386
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Kadowaki,N. and Liu,Y.J.
TITLE Dendritic cells; methods
JOURNAL Patent: WO 0234887-A 5 02-MAY-2002;
SCHERING CORPORATION (US)
FEATURES
source Location/Qualifiers
1..30
/organism="synthetic construct"
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/db_xref="taxon:32630"
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ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
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Db 1 ACCGATAACGTTGCCGGTGACG 22
|||||
RESULT 6
AX774078
LOCUS Sequence 3 from Patent WO03045431.
DEFINITION AX774078
ACCESSION AX774078
VERSION AX774078.1 GI:32485868
KEYWORDS
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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 other sequences; artificial sequences.
AUTHORS     Vicari,A.P. and Caux,C.
TITLE       Methods for treating cancer using a combination of a tumor-derived
            dendritic cell inhibitory factor antagonist and a toll-like
            receptor agonist
JOURNAL     Patent: WO 03045431-A 3 05-JUN-2003;
            SCHERING CORPORATION (US)
FEATURES    source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide"

ORIGIN
Query Match      100.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ACCGATAACGTTGCCGGTGACG 22
    |||||
Db   1 ACCGATAACGTTGCCGGTGACG 22

RESULT 7
AY858995
LOCUS      368 bp DNA linear BCT 16-JUN-2005
DEFINITION Mycobacterium avium complex strain MAIS-31 heat shock protein hsp65
            gene, partial cds.
ACCESSION  AY858995
VERSION     AY858995.1 GI:58004847
KEYWORDS    Mycobacterium avium complex
            Mycobacterium avium complex
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            avium complex (MAC).
REFERENCE   1 (bases 1 to 368)
AUTHORS     Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
            Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
            Herrmann,J.-L.
            Hsp65 sample MAIS 31
            Unpublished
            2 (bases 1 to 368)
            Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
            Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
            Herrmann,J.-L.
            Direct Submission
            Submitted (15-DEC-2004) Microbiologie, Hopital Saint Louis, 1
            avenue Claude Vellefaux, Paris 75010, France
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Query Match      92.7%; Score 20.4; DB 1; Length 368;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 other sequences; artificial sequences.
AUTHORS     Vicari,A.P. and Caux,C.
TITLE       Methods for treating cancer using a combination of a tumor-derived
            dendritic cell inhibitory factor antagonist and a toll-like
            receptor agonist
JOURNAL     Patent: WO 03045431-A 3 05-JUN-2003;
            SCHERING CORPORATION (US)
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DEFINITION Mycobacterium avium complex strain MAIS-31 heat shock protein hsp65
            gene, partial cds.
ACCESSION  AY858995
VERSION     AY858995.1 GI:58004847
KEYWORDS    Mycobacterium avium complex
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            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            avium complex (MAC).
REFERENCE   1 (bases 1 to 368)
AUTHORS     Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
            Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
            Herrmann,J.-L.
            Hsp65 sample MAIS 31
            Unpublished
            2 (bases 1 to 368)
            Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
            Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
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            Direct Submission
            Submitted (15-DEC-2004) Microbiologie, Hopital Saint Louis, 1
            avenue Claude Vellefaux, Paris 75010, France
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Query Match      92.7%; Score 20.4; DB 1; Length 368;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Vicari,A.P. and Caux,C.
TITLE       Methods for treating cancer using a combination of a tumor-derived
            dendritic cell inhibitory factor antagonist and a toll-like
            receptor agonist
JOURNAL     Patent: WO 03045431-A 3 05-JUN-2003;
            SCHERING CORPORATION (US)
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RESULT 7
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LOCUS   Mycobacterium avium complex strain MAIS-31 heat shock protein hsp65
DEFINITION
AUTHORS Herrmann,J.-L.
TITLE   Hsp65 sample MAIS 31
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 368)
AUTHORS Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
        Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Vicari,A.P. and Caux,C.
TITLE       Methods for treating cancer using a combination of a tumor-derived
            dendritic cell inhibitory factor antagonist and a toll-like
            receptor agonist
JOURNAL     Patent: WO 03045431-A 3 05-JUN-2003;
            SCHERING CORPORATION (US)
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LOCUS   Mycobacterium avium complex strain MAIS-31 heat shock protein hsp65
DEFINITION
AUTHORS Herrmann,J.-L.
TITLE   Hsp65 sample MAIS 31
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 368)
AUTHORS Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
        Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
        Herrmann,J.-L.
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Query Match      92.7%; Score 20.4; DB 1; Length 368;
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
Herrmann,J.-L.
Hsp65 sample MAIS 6
Unpublished
REFERENCE
AUTHORS
Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
Herrmann,J.-L.
Direct Submission
Submitted (15-DEC-2004) Microbiologie, Hopital Saint Louis, 1
avenue Claude Vellefaux, Paris 75010, France
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
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Db 37 ACCGACAACGTTGCCGGTGACG 58
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RESULT 11
AY859013 417 bp DNA linear BCT 16-JUN-2005
LOCUS
DEFINITION
Mycobacterium avium strain MAIS-25 heat shock protein hsp65 gene,
partial cds.
ACCESSION
AY859013
VERSION
AY859013.1 GI:58004883
KEYWORDS
Mycobacterium avium
SOURCE
Mycobacterium avium
ORGANISM
Mycobacterium avium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avium complex (MAC).
REFERENCE
1 (bases 1 to 417)
AUTHORS
Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
Herrmann,J.-L.
Hsp65 sample MAIS 25
Unpublished
REFERENCE
2 (bases 1 to 417)
AUTHORS
Lebrun,L., Weill,F.-X., Lafendi,L., Houriez,F., Casanova,F.,
Gutierrez,M.-C., Ingrand,D., Lagrange,P., Vincent,V. and
Herrmann,J.-L.
Direct Submission
Submitted (15-DEC-2004) Microbiologie, Hopital Saint Louis, 1
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 72 ACCGACAACGTTGCCGGTGACG 93
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RESULT 12
E04647 29 bp DNA linear PAT 29-SEP-1997
LOCUS
DEFINITION
Synthetic nucleotide with (GACGTC) structure, having immunomodulation
activities.

```

ACCESSION E04647
VERSION E04647.1 GI:2172843
KEYWORDS JP 1992352724-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 29)
AUTHORS Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O.,
Makino,T. and Shimada,S.
TITLE IMMUNOMODULATION TYPE THERAPEUTIC AGENT
JOURNAL Patent: JP 1992352724-A 4 07-DEC-1992;
MITSUI TOATSU CHEM INC
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992352724-A/4
PD 07-DEC-1992
PF 18-JUL-1991 JP 1991178058
PR 27-JUL-1990 JP 90P 197778
PI TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO
ETSURO,
PI YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
PC A61K31/70,A61K31/70,A61K31/70//C07H21/04;
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LOCUS A89781 30 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 3 from Patent WO9832462.
ACCESSION A89781
VERSION A89781.1 GI:6738295
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 3 30-JUL-1998;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
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A90868
LOCUS A90868 30 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 3 from Patent EP0855184.
ACCESSION A90868
VERSION A90868.1 GI:6739262
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Heeg,K.P. and Lipford,G.B.
TITLE Pharmaceutical composition comprising a polynucleotide and an
antigen especially for vaccination
JOURNAL Patent: EP 0855184-A 3 29-JUL-1998;
HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES
source
LOCATION/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 9.7e+02;
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DB 1 ACCGATGACGTCCCGGTGACG 22
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LOCUS BD056772 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Pharmaceutical composition comprising a polynucleotide and an
antigen especially for vaccination.
ACCESSION BD056772
VERSION BD056772.1 GI:22602378
KEYWORDS JP 2001508780-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Wagner,H., Lipford,G.B. and Heeg,K.
TITLE Pharmaceutical composition comprising a polynucleotide and an
antigen especially for vaccination
JOURNAL Patent: JP 2001508780-A 2 03-JUL-2001;
HERMANN WAGNER,GRAYSON B LIPFORD,KLAUS HEEG
COMMENT PN JP 2001508780-A/2
PD 03-JUL-2001
PF 23-JAN-1998 JP 1998531592
PR 23-JAN-1997 EP 97101019.4
PI HERMANN WAGNER,GRAYSON B LIPFORD,KLAUS HEEG
PC A61K39/39,A61K31/7088,A61K39/00,A61P37/04,C12N15/09,C12N15/00
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 01:23:12 ; Search time 165.506 Seconds
(without alignments)
885.910 Million cell updates/sec

Title: US-10-789-758A-3

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	22	3	AAC64138
3	22	100.0	22	4	AAF59503
4	22	100.0	22	4	AAH43896
5	22	100.0	22	5	AAF27749
6	22	100.0	30	2	AAQ20708
7	22	100.0	30	6	ABK85996
8	22	100.0	30	9	AA157122
9	22	100.0	30	10	ADC51790
10	22	100.0	30	13	ADQ16746
11	22	100.0	30	13	ADQ16813
12	22	100.0	30	13	ADW37971
13	22	100.0	93	13	ADW37977
14	22	100.0	1796	13	ADW37968
15	18.8	85.5	22	3	AA48594
16	18.8	85.5	22	2	AAQ20705
17	18.8	85.5	30	2	AAQ20707
18	18.8	85.5	30	2	AAQ20892
19	18.8	85.5	30	2	AAQ20881

20	18.8	85.5	30	2	AAQ20886	Aaq20886 Immunosti
21	18.8	85.5	30	2	AAQ20709	Aaq20709 Immunosti
22	18.8	85.5	30	2	AAQ20877	Aaq20877 Immunosti
23	18.8	85.5	30	2	AAV45994	Aav45994 Immune ad
24	18.8	85.5	30	2	AAV78804	Aav78804 HPV fusio
25	18.8	85.5	30	2	AAZ31945	Aaz31945 CpG adjuv
26	18.8	85.5	30	3	AAC60279	Aac60279 Immunosti
27	18.8	85.5	30	3	AAC64139	Aac64139 Immunosti
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29	18.8	85.5	30	4	AAF59507	Aaf59507 Immunosti
30	18.8	85.5	30	6	ABK85997	Abk85997 Dendritic
31	18.8	85.5	30	6	ABK85995	Abk85995 Dendritic
32	18.8	85.5	30	6	AA143436	Aa143436 Immunosti
33	18.8	85.5	30	6	ABV74425	Abv74425 Immunosti
34	18.8	85.5	30	6	ABN88304	Abn88304 Immunosti
35	18.8	85.5	30	6	ABL58455	Ab158455 CpG immu
36	18.8	85.5	30	8	ACC59108	Acc59108 CpG oligo
37	18.8	85.5	30	8	ABZ22868	Abz22868 Phosphoro
38	18.8	85.5	30	9	AA157123	Aa157123 Human tol
39	18.8	85.5	30	12	ADL64034	Adl64034 CpG DNA o
40	18.8	85.5	30	12	ADL63959	Adl63959 CpG DNA o
41	18.8	85.5	30	12	ADL97921	Adl97921 Immunosti
42	18.8	85.5	30	12	ADN11026	Adn11026 CpG oligo
43	18.8	85.5	30	12	ADQ07603	Adq07603 Urmethyla
44	18.8	85.5	30	13	ADU70012	Adu70012 Immunosti
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ALIGNMENTS

RESULT 1

AAA48593

ID AAA48593 standard; DNA; 22 BP.

XX

AC AAA48593;

XX

DT 20-SEP-2000 (first entry)

XX

DE Immunostimulatory oligonucleotide AAC-22.

XX

KW Replication protein A; immunostimulatory DNA; vaccine adjuvant;

KW immunotherapy; cancer; allergic disease; inflammatory disease;

KW inflammatory autoimmune disease; systemic lupus erythematosus; arthritis;

KW psoriasis; gingivitis; sarcoidosis; multiple sclerosis; colitis; ileitis;

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..21

FT /*tag= a

FT /note= "optionally phosphorothioate backbone"

XX

XX WO200031540-A1.

XX

XX 02-JUN-2000.

XX

XX 25-NOV-1999; 99WO-AU001052.

XX

XX 25-NOV-1998; 98AU-00007288.

XX (UYQU) UNIV QUEENSLAND.

XX

XX Stacey KJ, Sester DP, Sweet MJ, Hume DA;

XX WPI; 2000-400189/34.

XX

XX Detecting immunostimulatory DNA comprising contacting with replication

XX protein A (RPA) and detecting complex formation.

XX

XX Example 1; Page 28; 101pp; English.

XX

CC Replication protein A (RPA) is involved in a novel method for detecting
 CC immunostimulatory DNA. The method involves combining a sample of DNA with
 CC RPA and detecting complex formation. This method can be used to identify
 CC agonists and antagonists of immunostimulatory DNA. Agonists or
 CC antagonists may be used as vaccine adjuvants and for immunotherapy for
 CC cancer, allergic diseases, inflammatory diseases and inflammation
 CC autoimmune diseases (eg. systemic lupus erythematosus, arthritis,
 CC psoriasis, gingivitis, sarcoidosis, multiple sclerosis, colitis and
 CC ileitis). The present sequence is the immunostimulatory oligonucleotide
 CC AAC-22. This was used in the development of the novel method
 XX

SQ Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
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 Matches 22; Conservative 0; Indels 0;

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 Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 2

AAC64138
 ID AAC64138 standard; DNA; 22 BP.

XX AAC64138;

DT 19-FEB-2001 (first entry)

XX Immunostimulatory CpG oligonucleotide WD0003 used in an RSV vaccine.

XX Immunostimulatory oligonucleotide; CpG oligonucleotide;

KW respiratory syncytial virus; RSV; vaccine; phosphorothioate;
 KW unmethylated; adjuvant; ss.

XX Synthetic.

XX WO200062802-A2.

XX 26-OCT-2000.

XX 17-APR-2000; 2000WO-EP003516.

XX 20-APR-1999; 99GB-00009077.

XX 28-JUN-1999; 99GB-00015106.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Deschamps M;

XX WPI; 2000-679550/66.

XX Novel vaccine formulation comprising a respiratory syncytial virus (RSV)
 PT antigen and an immunostimulatory CpG oligonucleotide useful for treating
 PT RSV infections mutations.

XX Claim 9; Page 26; 34pp; English.

XX The invention relates to a novel vaccine formulation comprising a
 CC respiratory syncytial virus (RSV) antigen and an immunostimulatory CpG
 CC oligonucleotide. The CpG motifs of the immunostimulatory oligonucleotide
 CC are unmethylated, and the backbone of the oligonucleotide is preferably
 CC all-phosphorothioate. The RSV antigen used may be F (fusion) protein, G
 CC (attachment) protein, an FG fusion protein, an immunogenic derivative of
 CC any of these proteins, or inactivated RSV. RSV causes lower respiratory
 CC tract illness in humans, particularly in children and the elderly. The
 CC RSV vaccine of the invention is used for preventing or ameliorating RSV
 CC infection in a patient. The present sequence represents an
 CC immunostimulatory CpG oligonucleotide which may be used in the RSV
 CC vaccine of the invention

XX Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Gaps 0;
 Matches 22; Conservative 0; Indels 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
 |||||
 Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 3

AAF59503
 ID AAF59503 standard; DNA; 22 BP.

XX AAF59503;

XX 24-APR-2001 (first entry)

XX Immunostimulatory CpG oligonucleotide WD1003 for use in an HIV vaccine.

XX Immunostimulatory CpG oligonucleotide; adjuvant; HIV antigen;

KW HIV infection; vaccine; prophylaxis; treatment; ss.

XX Synthetic.

XX WO200100232-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-EP005998.

XX 29-JUN-1999; 99GB-00015205.

XX 31-JAN-2000; 2000GB-00002200.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Garcon N, Voss G;

XX WPI; 2001-122974/13.

XX New vaccine formulation comprising human immunodeficiency virus (HIV)
 PT antigen and immunostimulatory CpG oligonucleotide, useful for preventing
 PT and treating HIV infections in a patient.

XX Claim 10; Page 17; 23pp; English.

XX The invention relates to an HIV vaccine comprising an HIV antigen and an
 CC immunostimulatory oligonucleotide (AAF59501-AAF59508). With the exception
 CC of oligonucleotide WD1005 (AAF59505), the immunostimulatory
 CC oligonucleotides contain at least one unmethylated CpG motif. In
 CC preferred embodiments the internucleotide linkage is phosphorodithioate,
 CC although phosphodiester and other internucleotide bonds, or mixtures of
 CC linkages are within the scope of the invention. The HIV antigen may be
 CC selected from gp160, gp120, Nef, Tat, and Nef or Tat derivatives or
 CC fusion proteins. The vaccine is used for the prophylaxis or treatment of
 CC HIV infection in a patient. The present sequence represents a
 CC specifically claimed immunostimulatory CpG oligonucleotide for use in the
 CC vaccine of the invention

XX Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Gaps 0;
 Matches 22; Conservative 0; Indels 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
 |||||
 Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 4

AAH43896
 ID AAH43896 standard; DNA; 22 BP.

```

XX AAH43896;
AC
XX
XX
DT 04-SEP-2001 (first entry)
XX
XX
DE Human hsp60 related immunostimulatory oligonucleotide #1.
XX
XX Human; heat shock protein; hsp60; inhibition; antagonist; antiallergic;
KW pro-inflammatory immune response; immune system; inflammatory disease;
KW immunostimulatory; antiinflammatory; antidiabetic; immunosuppressive;
KW antirheumatic; nontropic; antiarteriosclerotic; antimicrobial; antiulcer;
KW neuroprotective; autoimmune disease; diabetes; multiple sclerosis;
KW rheumatoid arthritis; myasthenia gravis; systemic lupus erythematosus;
KW chronic inflammation; atherosclerosis; inflammatory bowel disease;
KW reactive arthritis; chronic infection; graft rejection; gingivitis;
KW gastritis; ulcer; thrombosis; allergy; acute infection; ss.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200143691-A2.
XX
XX 21-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-IL000833.
XX
XX 15-DEC-1999; 99EP-00125035.
XX
XX 15-DEC-1999; 99US-0172297P.
XX
XX (PEPT-) PEPTOR LTD.
XX
XX Kolb H, Elias D;
PI
XX
XX WPI; 2001-390150/41.
XX
XX Anti-inflammatory peptides of hsp60, which are capable of acting as
PT antagonists of hsp60, useful for treating an inflammatory disease or
PT disorder, e.g. an autoimmune disease, diabetes, multiple sclerosis and
PT rheumatoid arthritis.
XX
XX Example 1; Page 40; 76pp; English.
XX
XX The present invention describes anti-inflammatory peptides of heat shock
CC protein hsp60, which are capable of acting as antagonists of hsp60
CC characterised by their ability to reduce or prevent the induction of a
CC pro-inflammatory immune response of cells of the innate immune system by
CC hsp60. The peptides have antiinflammatory, antidiabetic, antirheumatic,
CC immunosuppressive, nontropic, antiarteriosclerotic, antimicrobial,
CC antiulcer, antiallergic and neuroprotective activities. The antagonists
CC are useful in the treatment of an inflammatory disease or disorder, e.g.
CC an autoimmune disease, diabetes, multiple sclerosis, rheumatoid
CC arthritis, myasthenia gravis, systemic lupus erythematosus, chronic
CC inflammation, atherosclerosis, inflammatory bowel disease, reactive
CC arthritis, chronic infections, graft rejection, gingivitis, gastritis,
CC ulcer, thrombosis, allergy and acute infections. AAH43896 to AAH43899 and
CC AAB9542 to AAB95673 represent sequences used in the exemplification of
CC the present invention
XX
XX Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGATACGTTGCCGGTGACG 22
Db |||||
1 ACCGATACGTTGCCGGTGACG 22

RESULT 5
AAH43896
ID AAF27749 standard; DNA; 22 BP.
XX

```

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AC AAF27749;
XX
XX 03-APR-2001 (first entry)
XX
XX P. falciparum vaccine CpG oligonucleotide WD1003.
XX
XX Plasmodium falciparum; malaria; CpG oligonucleotide; vaccine; sporozoite;
KW ds.
XX
XX Unidentified.
OS
XX WO200100231-A2.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-EP005841.
XX
XX 29-JUN-1999; 99GB-00015204.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cohen J, Garcon N, Voss G;
PI
XX WPI; 2001-112392/12.
XX
XX New vaccine formulation, useful for preventing and treating plasmodium
PT infection in a patient, comprises malaria antigen and immunostimulatory
PT CpG oligonucleotide.
XX
XX Claim 8; Page 16; 22pp; English.
XX
XX The present invention describes a vaccine comprising a malaria antigen
CC and an immunostimulatory CpG oligonucleotide. This is useful in the
CC prevention and treatment of malaria caused by Plasmodium falciparum
CC infection
XX
XX Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGATACGTTGCCGGTGACG 22
Db |||||
1 ACCGATACGTTGCCGGTGACG 22

RESULT 6
AAQ20708
ID AAQ20708 standard; DNA; 30 BP.
XX
XX AAQ20708;
XX
XX 11-MAY-1992 (first entry)
XX
XX Immunostimulatory oligonucleotide #6 contg. palindrome.
XX
XX Natural killer cell; NK; immunodeficiency; autoimmune disease; CSP;
KW anti-tumour; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX misc_feature 7..12
FT /*tag= a
FT /note= "palindrome, i.e. complementary strand sequence is
FT identical reading 5'-3'"
XX
XX EP468520-A.
XX
XX 29-JAN-1992.
XX
XX 27-JUL-1990; 90JP-00197778.
XX

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XX PR 27-JUL-1990; 90JP-00197778.
XX PA (MITK ) MITSUI TOATSU CHEM INC.
XX PI Tokunaga T, Katsoka T, Yamamoto S, Kuramoto E, Yano O, Shimada S;
XX PI Makino T;
XX WI 1992-034272/05.
XX DR Immunostimulants contg. palindromic DNA - enhance interferon, macrophage
XX PT activating factor and colony stimulating factor and promote lymphocyte
XX PT proliferation.
XX PS Claim 12; Page 25; 45pp; English.
XX CC This single-stranded oligonucleotide is one example of an
XX CC immunostimulatory sequence containing a palindrome. The sequence is very
XX CC similar to the sequence of the first 30 nucleotides of an
XX CC immunostimulatory 45mer (see AAQ20698) but has a different palindromic
XX CC sequence. It has a strong activity to augment the activity of mouse NK
XX CC cells
XX SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
DB 1 ACCGATAACGTTGCCGGTGACG 22
RESULT 7
ABK85996
ID ABK85996 standard; DNA; 30 BP.
XX AC ABK85996;
XX DT 21-AUG-2002 (first entry)
XX DE Dendritic cell stimulating oligodeoxynucleotide AAC-30.
XX KW Oligodeoxynucleotide; ODN; dendritic cell stimulation; ss; hepatitis;
XX KW interferon producing cell; CpG; antiviral; anti-HIV; cytostatic;
XX KW dendritic cell maturation; viral infection; HIV; tumour;
XX KW human immunodeficiency virus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..30
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphodiester backbone"
XX FT misc_feature 7..12
XX FT /*tag= b
XX FT /note= "Palindromic sequence"
XX PN WO200234887-A2.
XX PD 02-MAY-2002.
XX XX 22-OCT-2001; 2001WO-US047529.
XX XX 24-OCT-2000; 2000US-0243232P.
XX PA (SCHE ) SCHERING CORP.
XX PI Kadowaki N, Liu Y;
XX WI 2002-489942/52.
XX DR
XX XX Inducing maturation of an interferon producing cell (IPC) to a dendritic
XX PT cell or inducing interferon alpha production, for e.g. therapy of tumors,
XX PT comprises contacting the IPC with a CpG nucleic acid.
XX PS Claim 4; Page 15; 24pp; English.
XX CC This invention relates to a novel method for inducing maturation of an
XX CC interferon producing cell to a dendritic cell and inducing interferon
XX CC alpha (IFN alpha) production by the interferon producing cell upon viral
XX CC stimulation. The method comprises contacting the interferon producing
XX CC cell with a CpG nucleic acid. The method of the invention may have
XX CC antiviral, anti-HIV or cytostatic activities. The method of the invention
XX CC is useful for modulating the physiology of certain defined subsets of
XX CC dendritic cells, as well as for regulating the production of various
XX CC interferons by subsets of dendritic cells. Specifically, the methods of
XX CC the invention are useful for inducing IFN alpha production, IL-12
XX CC production, and interferon producing cell or dendritic cell maturation.
XX CC The interferon producing cells are useful in cellular therapy for viral
XX CC infections and diseases such as human immunodeficiency virus (HIV),
XX CC hepatitis and tumours. The present sequence represents an
XX CC oligodeoxynucleotide used in the method of the invention
XX SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
DB 1 ACCGATAACGTTGCCGGTGACG 22
RESULT 8
AAL57122
ID AAL57122 standard; DNA; 30 BP.
XX AC AAL57122;
XX DT 17-SEP-2003 (first entry)
XX DE Human toll-like receptor (TLR) 9 agonist oligonucleotide AAC-30.
XX KW Cancer; tumour; dendritic cell; Toll-like receptor; TLR; cytostatic;
XX KW AAC-30; CpG; human; ss.
XX OS Synthetic.
XX PN WO2003045431-A2.
XX PD 05-JUN-2003.
XX PF 26-NOV-2002; 2002WO-US038098.
XX PR 27-NOV-2001; 2001US-0333434P.
XX PA (SCHE ) SCHERING CORP.
XX PI Vicari AP, Caux C;
XX WI 2003-493377/46.
XX DR Treating cancer, involves administering tumor-derived dendritic cell
XX PT inhibitory factor antagonist in combination with Toll-like receptor
XX PT agonist, to an individual in need of the treatment.
XX PS Claim 12; Page 16; 47pp; English.
XX CC This invention relates to a novel method of treating cancer and comprises
XX CC the administration of an effective amount of a tumour-derived dendritic
XX CC cell (DC) inhibitory antagonist in combination with an effective amount
XX CC of Toll-like receptor (TLR) agonist to an individual in need of

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CC treatment. The method has cytostatic activity through the activation of
CC dendritic cells that are rendered hypo-responsive to activation stimuli
CC by the disease. The method is useful for treating cancers such as
CC melanoma, breast, pancreas, colon, lung, glioma, hepatocellular,
CC endometrium, gastric, intestinal, renal, prostate, thyroid, ovarian,
CC testicular, liver, head and neck, colorectal, esophagus, stomach, eye,
CC bladder, glioblastoma and metastatic carcinomas. The present sequence is
CC that of CpG motif-containing unmethylated oligonucleotide AAC-30 of the
CC invention, an agonist of Toll-like receptor (TLR) 9 and which is active
CC on human dendritic cells

SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.9;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22

Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 9

ADCS1790

ID ADC51790 standard; DNA; 30 BP.

XX AC ADC51790;

XX 18-DEC-2003 (first entry)

XX AAC-30 SEQ ID NO:3.

XX ds; TLR7; immunopotentiating synthetic compound; virucide; TRL agonist;
KW TRL antagonist; imidazoquinoline compound; viral infection; AAC-30.

XX Synthetic.

XX WO2003043588-A1.

XX 30-MAY-2003.

XX 22-NOV-2002; 2002WO-JP012234.

XX 22-NOV-2001; 2001JP-00358295.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (AKIR/) AKIRA S.

XX Akira S, Tomizawa H, Yamaoka T;

XX WPI; 2003-513577/48.

XX Non-human model animals unresponsive to an immunopotentiating synthetic
PT compound e.g. of imidazoquinoline type lacking TLR7-encoded gene
PT function, useful in screening drugs.

XX Disclosure; Page 22; 59pp; Japanese.

XX The invention relates to a novel non-human model animal unresponsive to
CC an immunopotentiating synthetic compound, characterised by lacking a gene
CC function that encodes TLR7 which recognises an immunopotentiating
CC synthetic compound. a polynucleotide of the invention has virucide
CC activity, and is useful as a TRL agonist and TRL antagonist. The model
CC animals are useful in studying the mechanism of action of
CC imidazoquinoline compounds, and in screening remedies particularly
CC synthetic compounds for viral infections. The present sequence is used in
CC the invention.

SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 10; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.9;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22

Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 10

ADQ16746

ID ADQ16746 standard; DNA; 30 BP.

XX AC ADQ16746;

XX 07-OCT-2004 (first entry)

XX Immunomodulatory polynucleotide, SEQ ID NO 25.

XX Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
KW trinucleotide; antimicrobial; anti-allergic; antiasthmatic;
KW dermatological; anti-inflammatory; ophthalmological; immunosuppressive;
KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
KW anti-HIV; cytostatic; antiulcer; nephrotropic; IGF-related disorder;
KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.

XX Unidentified.

XX WO2004058179-A2.

XX 15-JUL-2004.

XX 18-DEC-2003; 2003WO-US041001.

XX 23-DEC-2002; 2002US-0436122P.

XX 13-FEB-2003; 2003US-0447885P.

XX 01-MAY-2003; 2003US-0467546P.

XX (DYNA-) DYNAVAX TECHNOLOGIES.

XX Dina D, Fearon KL, Marshall J;

XX WPI; 2004-525782/50.

XX Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
PT dermatitis comprises palindromic sequence comprising at least eight bases
PT in length, which contains at least two dinucleotides and at least one
PT trinucleotide.

XX Disclosure; SEQ ID NO 25; 119pp; English.

XX The invention relates to a novel immunomodulatory polynucleotide (IMP)
CC comprising a palindromic sequence. The palindromic sequence comprises at
CC least 8 bases in length, which contains at least two dinucleotides (CG),
CC and at least one trinucleotide (TCG) at or near the 5' end of the
CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
CC of the (TCG) is positioned 0 - 3 bases from the 5' end of the
CC polynucleotide. The (TCG) is separated from the 5' end of the
CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
CC all or part of the (TCG) sequence, where y= 1 or 2. The immunomodulatory
CC polynucleotides have the following activities: antimicrobial,
CC anti-allergic, antiasthmatic, dermatological, antiinflammatory,
CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
CC and nephrotropic. The immunomodulatory polynucleotides can be used for
CC ameliorating a symptom of an infectious disease and IGF-related disorder.
CC The IMP's may also be used for the treatment of a disorder associated
CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
CC induced asthma or atopic dermatitis), individuals receiving vaccines such
CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
CC mycobacterial epitope or a tumour associated epitope) or prophylactic
CC vaccines. The IMP's can also be used for the treatment of e.g. food
CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,

CC Hymenoptera sting allergies and drug allergies and parasitic infections;
 CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
 CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
 CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
 CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
 CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
 CC fibrosis, renal fibrosis. The IMP's may also be used to create a
 CC prophylactic vaccine to increase resistance to infection by bacterial or
 CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
 CC response; or increases interferon-gamma; or interferon-alpha; effectively
 CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
 CC omega and IFN-gamma, production from human cells; effectively stimulates
 CC B cells to proliferate; and activates plasmacytoid dendritic cells to
 CC undergo maturation which can result in retardation of plasmacytoid
 CC dendritic cell apoptosis in culture. This polynucleotide sequence
 CC represents an immunomodulatory polynucleotide of the invention.
 XX
 SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 22; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGATAACGTTGCCGGTGACG 22
 Db 1 ACCGATAACGTTGCCGGTGACG 22
 RESULT 11
 ADQ16813
 ID ADQ16813 standard; DNA; 30 BP.
 AC ADQ16813;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Immunomodulatory polynucleotide, SEQ ID No 92.
 XX
 KW Immunomodulatory polynucleotide; IMP; palindromic sequence; dinucleotide;
 KW trinucleotide; antimicrobial; anti-allergic; antiasthmatic;
 KW dermatological; antiinflammatory; ophthalmological; immunosuppressive;
 KW antibacterial; vasotropic; antiparasitic; virucide; hepatotropic;
 KW anti-HIV; cytostatic; antiulcer; nephrotropic; IgE-related disorder;
 KW T helper; (TH)2-type immune response; vaccine; prophylactic; immune;
 KW interferon-gamma; interferon-alpha; type I interferon; IFN-alpha;
 KW IFN-omega; IFN-gamma; plasmacytoid dendritic cell; ss.
 XX
 OS Unidentified.
 XX
 MO2004058179-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 18-DEC-2003; 2003WO-US041001.
 XX
 PR 23-DEC-2002; 2002US-0436122P.
 PR 13-FEB-2003; 2003US-0447885P.
 PR 01-MAY-2003; 2003US-0467546P.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES.
 XX
 PI Dina D, Fearon KL, Marshall J;
 XX
 WI; 2004-525782/50.
 XX
 DR Immunomodulatory polynucleotide useful for the treatment of e.g. atopic
 PT dermatitis comprises palindromic sequence comprising at least eight bases
 PT in length, which contains at least two dinucleotides and at least one
 PT trinucleotide.
 XX
 Example 1; SEQ ID NO 92; 119pp; English.
 XX
 The invention relates to a novel immunomodulatory polynucleotide (IMP)

CC comprising a palindromic sequence. The palindromic sequence comprises at
 CC least 8 bases in length, which contains at least two dinucleotides (CG),
 CC and at least one trinucleotide (TCG) at or near the 5' end of the
 CC polynucleotide. The CG dinucleotides are separated by 0 - 5 bases. The 5'
 CC T of the (TCG) is positioned 0 - 3 bases from the 5' end of the
 CC polynucleotide. The (TCG) is separated from the 5' end of the
 CC palindromic sequence by 0 - 2 bases. The palindromic sequence includes
 CC all or part of the (TCG) sequence, where Y= 1 or 2. The immunomodulatory
 CC polynucleotides have the following activities: antimicrobial,
 CC anti-allergic, antiasthmatic, dermatological, antiinflammatory,
 CC ophthalmological, immunosuppressive, antibacterial, vasotropic,
 CC antiparasitic, virucide, hepatotropic, anti-HIV, cytostatic, antiulcer,
 CC and nephrotropic. The immunomodulatory polynucleotides can be used for
 CC ameliorating a symptom of an infectious disease and IgE-related disorder.
 CC The IMP's may also be used for the treatment of a disorder associated
 CC with a T helper (TH)2-type immune response (e.g. allergies, allergy-
 CC induced asthma or atopic dermatitis), individuals receiving vaccines such
 CC as therapeutic vaccines (e.g. vaccines comprising an allergy epitope, a
 CC mycobacterial epitope or a tumour associated epitope) or prophylactic
 CC vaccines. The IMP's can also be used for the treatment of e.g. food
 CC allergies, rhinitis, atopic dermatitis, conjunctivitis, urticaria, shock,
 CC Hymenoptera sting allergies and drug allergies and parasitic infections;
 CC viral disease e.g. Hepatitis B, Hepatitis C, influenza, Acquired
 CC immunodeficiency syndrome (AIDS) and Herpes zoster; and cancer;
 CC inflammatory disorder e.g. ulcerative colitis; fibrotic disorder e.g.
 CC idiopathic pulmonary fibrosis, scleroderma, cutaneous radiation-induced
 CC fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic
 CC fibrosis, renal fibrosis. The IMP's may also be used to create a
 CC prophylactic vaccine to increase resistance to infection by bacterial or
 CC viral pathogens. The immunomodulatory polynucleotide modulates an immune
 CC response; or increases interferon-gamma; or interferon-alpha; effectively
 CC stimulates cytokines including type I interferons e.g. IFN-alpha and IFN-
 CC omega and IFN-gamma, production from human cells; effectively stimulates
 CC B cells to proliferate; and activates plasmacytoid dendritic cells to
 CC undergo maturation which can result in retardation of plasmacytoid
 CC dendritic cell apoptosis in culture. This polynucleotide sequence
 CC represents an immunomodulatory polynucleotide of the invention.
 XX
 SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 22; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGATAACGTTGCCGGTGACG 22
 Db 1 ACCGATAACGTTGCCGGTGACG 22
 RESULT 12
 ADW37971
 ID ADW37971 standard; DNA; 30 BP.
 AC ADW37971;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE ODN plasmid related oligonucleotide #3.
 XX
 KW ss; vaccine; hepatitis B; infection; cancer; cytostatic neoplasm;
 KW virucide; antiinflammatory; hepatotropic; gastrointestinal disease.
 XX
 OS Homo sapiens.
 XX
 PN CN1468957-A.
 XX
 PD 21-JAN-2004.
 XX
 PF 19-JUL-2002; 2002CN-00136125.
 XX
 PR 19-JUL-2002; 2002CN-00136125.
 XX
 PA (UYMI-) UNIV MILITARY MEDICAL NO 2 PLA.

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XX Zhao P, Qi Z;
PI WPI; 2004-270526/26.
DR Plasmid used as human therapeutic vaccine adjuvant.
XX Claim 3; Page 2; 9pp; Chinese.
XX The present invention provides one kind of high-copied and stable
CC plasmid, which is prepared through combining oligonucleotide sequence ODN
CC with immunostimulation to specific vector. The ODN inside the plasmid can
CC stimulate immune cell without being modified with thiophosphate. The
CC plasmid may be used as immune adjuvant and especially as adjuvant of
CC therapeutic vaccine for treating hepatitis B and other chronic contagious
CC diseases and tumors. The present sequence represents an ODN plasmid
CC related oligonucleotide.
XX Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
DB 1 ACCGATAACGTTGCCGGTGACG 22
RESULT 13
ADW37977
ID ADW37977 standard; DNA; 93 BP.
AC ADW37977;
XX 10-MAR-2005 (first entry)
DT ODN plasmid related oligonucleotide #5.
DE ss; vaccine; hepatitis B; infection; cancer; cytostatic neoplasm;
KW virucide; antiinflammatory; hepatotropic; gastrointestinal disease.
XX Homo sapiens.
XX CN1468957-A.
XX 21-JAN-2004.
XX 19-JUL-2002; 2002CN-00136125.
XX 19-JUL-2002; 2002CN-00136125.
XX (UYMI-) UNIV MILITARY MEDICAL NO 2 PLA.
XX Zhao P, Qi Z;
PI WPI; 2004-270526/26.
DR Plasmid used as human therapeutic vaccine adjuvant.
XX Disclosure; Page 7; 9pp; Chinese.
XX The present invention provides one kind of high-copied and stable
CC plasmid, which is prepared through combining oligonucleotide sequence ODN
CC with immunostimulation to specific vector. The ODN inside the plasmid can
CC stimulate immune cell without being modified with thiophosphate. The
CC plasmid may be used as immune adjuvant and especially as adjuvant of
CC therapeutic vaccine for treating hepatitis B and other chronic contagious
CC diseases and tumors. The present sequence represents an ODN plasmid
CC related oligonucleotide.
XX Sequence 93 BP; 17 A; 20 C; 40 G; 16 T; 0 U; 0 Other;
SQ
```

```
Query Match 100.0%; Score 22; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
DB 68 ACCGATAACGTTGCCGGTGACG 89
RESULT 14
ADW37968
ID ADW37968 standard; DNA; 1796 BP.
XX ADW37968;
AC 10-MAR-2005 (first entry)
DT ODN plasmid related DNA.
DE ds; gene; vector; vaccine; hepatitis B; infection; cancer;
KW cytostatic neoplasm; virucide; antiinflammatory; hepatotropic;
KW gastrointestinal disease.
XX Homo sapiens.
XX CN1468957-A.
XX 21-JAN-2004.
XX 19-JUL-2002; 2002CN-00136125.
XX 19-JUL-2002; 2002CN-00136125.
XX (UYMI-) UNIV MILITARY MEDICAL NO 2 PLA.
XX Zhao P, Qi Z;
PI WPI; 2004-270526/26.
DR Plasmid used as human therapeutic vaccine adjuvant.
XX Claim 6; SEQ ID NO 1; 9pp; Chinese.
XX The present invention provides one kind of high-copied and stable
CC plasmid, which is prepared through combining oligonucleotide sequence ODN
CC with immunostimulation to specific vector. The ODN inside the plasmid can
CC stimulate immune cell without being modified with thiophosphate. The
CC plasmid may be used as immune adjuvant and especially as adjuvant of
CC therapeutic vaccine for treating hepatitis B and other chronic contagious
CC diseases and tumors. The present sequence represents ODN plasmid related
CC DNA.
XX Sequence 1796 BP; 367 A; 553 C; 528 G; 348 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 13; Length 1796;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
DB 51 ACCGATAACGTTGCCGGTGACG 72
RESULT 15
AAA48594
ID AAA48594 standard; DNA; 22 BP.
XX AAA48594;
AC 20-SEP-2000 (first entry)
DT Immunostimulatory oligonucleotide ACC-22.
XX
```

KW Replication protein A; immunostimulatory DNA; vaccine adjuvant;
KW immunotherapy; cancer; allergic disease; inflammatory disease;
KW inflammatory autoimmune disease; systemic lupus erythematosus; arthritis;
KW psoriasis; gingivitis; sarcoidosis; multiple sclerosis; colitis; ileitis;
KW ss.
XX
XX
OS Synthetic.
XX
PN WO200031540-A1.
XX
PD 02-JUN-2000.
XX
XX
PF 25-NOV-1999; 99WO-AU001052.
XX
PR 25-NOV-1998; 98AU-00007288.
XX
XX (UYQU) UNIV QUEENSLAND.
XX
PI Stacey KJ, Sester DP, Sweet MJ, Hume DA;
XX
XX WPI; 2000-400189/34.
XX
XX
PT Detecting immunostimulatory DNA comprising contacting with replication
PT protein A (RPA) and detecting complex formation.
XX
XX Example 1; Page 28; 101pp; English.
XX
XX Replication protein A (RPA) is involved in a novel method for detecting
CC immunostimulatory DNA. The method involves combining a sample of DNA with
CC RPA and detecting complex formation. This method can be used to identify
CC agonists and antagonists of immunostimulatory DNA. Agonists or
CC antagonists may be used as vaccine adjuvants and for, immunotherapy for
CC cancer, allergic diseases, inflammatory diseases and inflammation
CC autoimmune diseases (eg. systemic lupus erythematosus, arthritis,
CC psoriasis, gingivitis, sarcoidosis, multiple sclerosis, colitis and
CC ileitis). The present sequence is the immunostimulatory oligonucleotide
CC ACC-22. This was used in the development of the novel method
XX
SQ Sequence 22 BP; 4 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 3; Length 22;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTCCCGTGACG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACCGATACCGTGCCTGACG 22
| | | | | | | | | | | | | | | | | | | | | |

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:45:02 ; Search time 1559.34 Seconds
(without alignments)
660.095 Million cell updates/sec

Title: US-10-789-758A-3

Perfect score: 22
Sequence: 1 accgataacgttgcggtagc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gse1: *
10: gb_gse2: *
11: gb_gse3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18.4	83.6	814	10	CG441696	CG441696 OGVHP85TH
2	18.4	83.6	860	10	CZ308727	CZ308727 ZMMPF0005
3	18.4	83.6	1025	10	CL455084	CL455084 ZMMPB048
4	18.4	83.6	1141	10	CG752100	CG752100 P046-3-H1
5	18.4	83.6	1354	10	CG755877	CG755877 P051-2-C1
6	17.8	80.9	410	11	CT022132	CT022132 KBrH133M0
7	17.8	80.9	670	10	CZ831026	CZ831026 OC_Ba021
8	17.8	80.9	969	9	CC850938	CC850938 NDL10902
9	17.8	80.9	1202	8	DN693955	DN693955 CGX91-D12
10	17.4	79.1	203	6	CD847930	CD847930 DHOAB672C
11	17.4	79.1	266	6	CD852670	CD852670 DHOALL82A
12	17.4	79.1	334	10	CW511638	CW511638 Shotgun_P
13	17.4	79.1	341	10	CW511977	CW511977 Shotgun_P
14	17.4	79.1	384	2	BES23578	BES23578 M38H38TM
15	17.4	79.1	387	3	BP825967	BP825967 BP825967
16	17.4	79.1	606	5	BX838137	BX838137 BX838137
17	17.4	79.1	631	8	CX942778	CX942778 LamjGeat3
18	17.4	79.1	647	6	CB257116	CB257116 45-E01274
19	17.4	79.1	648	6	CA103306	CA103306 SCEZHR104
20	17.4	79.1	654	5	BU014814	BU014814 QGJ8R09.y
21	17.4	79.1	663	1	AV823063	AV823063 AV823063
22	17.4	79.1	670	5	BU010172	BU010172 QGJ12K14.

23	17.4	79.1	732	5	BU012310	BU012310 QGJ1J08.y
24	17.4	79.1	744	5	BU014761	BU014761 QGJBE16.y
25	17.4	79.1	745	5	BQ850661	BQ850661 QGB13D16.
c 26	17.4	79.1	749	3	BM493093	BM493093 LIT000010
c 27	17.4	79.1	749	5	BU038321	BU038321 LIT000227
28	17.4	79.1	751	8	DR619320	DR619320 EST100944
29	17.4	79.1	767	6	CD855696	CD855696 DHOAF232A
30	17.4	79.1	777	6	CD853832	CD853832 DHOANM222
31	17.4	79.1	783	5	BX837439	BX837439 BX837439
32	17.4	79.1	963	5	BX837075	BX837075 BX837075
33	17.4	79.1	1326	4	CNS0A34P	BX826451 Arabidops
34	17.4	79.1	1380	4	CNS0A352	BX826636 Arabidops
35	17.4	79.1	1403	4	CNS0A2Z4	BX828114 Arabidops
36	17.4	79.1	1415	4	CNS0A33W	BX827739 Arabidops
37	17.4	79.1	1457	4	CNS0A3BP	BX826309 Arabidops
c 38	17.4	79.1	3558	10	CL944005	CL944005 OeIFSB001
39	17.2	78.2	317	8	DR911285	DR911285 USDA-FP.1
c 40	17.2	78.2	403	1	AV633400	AV633400 AV633400
c 41	17.2	78.2	430	7	CO909188	CO909188 BJ0204280
c 42	17.2	78.2	495	8	CX715565	CX715565 RTPQ1_35
c 43	17.2	78.2	500	1	AV636859	AV636859 AV636859
c 44	17.2	78.2	515	1	AV395473	AV395473 AV395473
c 45	17.2	78.2	535	1	AV392702	AV392702 AV392702

ALIGNMENTS

RESULT 1
CG441696
LOCUS OGVHP85TH ZM_0.7_1.5 KB Zea mays genomic clone ZMMBma0485002, linear GSS 17-SEP-2003
DEFINITION genomic survey sequence.
ACCESSION CG441696
VERSION CG441696.1 GI:34820175
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OGVHP85TV
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
FEATURES
Location/Qualifiers
1..814
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0485002"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 83.6%; Score 18.4; DB 10; Length 814;
Best Local Similarity 95.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGATACGTTGCCGGTGAC 21

```

Db      383 CCGATAACTTTGCCGGTGAC 402
||||||| ||||||| ||||||| |||
||||||| ||||||| ||||||| |||

RESULT 2
CZ308727      860 bp      DNA      linear      GSS 24-MAR-2005
LOCUS      ZMMBF0005017r ZMMBF Zea mays genomic clone ZMMBF0005017 3', genomic
DEFINITION      survey sequence.
ACCESSION      CZ308727
VERSION      CZ308727.1 GI:61747428
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 860)
REFERENCE      Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.,
AUTHORS      and Messing,J.
TITLE      Construction, Sequencing and Characterization of a Fosmid Library
JOURNAL      Of the B73 Maize Genome
COMMENT      Unpublished (2005)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: Fos_R
Class: Fosmid ends.
Location/Qualifiers
1. .860
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBF0005017"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBB"
/note="Vector: pEpiPOS-5; Site_1: Eco72I"

ORIGIN
Query Match      83.6%; Score 18.4; DB 10; Length 860;
Best Local Similarity 95.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGATAACGTTGCCGGTGAC 21
||||||| ||||||| ||||||| |||
Db      134 CCGATAACTTTGCCGGTGAC 153
||||||| ||||||| ||||||| |||

RESULT 3
CL455084      1025 bp      DNA      linear      GSS 29-MAR-2004
LOCUS      ZMMBB0482D20f ZMMBB (HindIII) Zea mays genomic clone
DEFINITION      ZMMBB0482D20 5', genomic survey sequence.
ACCESSION      CL455084
VERSION      CL455084.1 GI:45781435
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1025)
REFERENCE      Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
AUTHORS      Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE      Sequencing of the maize genome at FGIR (2003c)
JOURNAL      Unpublished (2003)
COMMENT      Contact: Bharti,A.K.

FEATURES
source
1. .1141
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match      83.6%; Score 18.4; DB 10; Length 1141;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGATAACGTTGCCGGTGAC 21
||||||| ||||||| ||||||| |||
Db      312 CCGATAACTTTGCCGGTGAC 331
||||||| ||||||| ||||||| |||

RESULT 4
CG752100      1141 bp      DNA      linear      GSS 24-OCT-2003
LOCUS      P046-3-Hli.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
DEFINITION      genomic survey sequence.
ACCESSION      CG752100
VERSION      CG752100.1 GI:37975230
KEYWORDS      GSS.
SOURCE      Pristionchus pacificus
ORGANISM      Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1141)
REFERENCE      Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
AUTHORS      Buntjer,J., van der Meulen,M. and Sommer,R.U.
TITLE      An integrated physical and genetic map of the nematode Pristionchus
JOURNAL      pacificus
PUBMED      Mol. Genet. Genomics 269 (5), 715-722 (2003)
COMMENT      Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1. .1141
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match      83.6%; Score 18.4; DB 10; Length 1141;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 121.
Location/Qualifiers
1. .1025
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0482D20"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBB"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

FEATURES
source
1. .1025
/organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
/clone="ZMMBB0482D20"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBB"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      83.6%; Score 18.4; DB 10; Length 1025;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGATAACGTTGCCGGTGAC 21
||||||| ||||||| ||||||| |||
Db      312 CCGATAACTTTGCCGGTGAC 331
||||||| ||||||| ||||||| |||

RESULT 4
CG752100      1141 bp      DNA      linear      GSS 24-OCT-2003
LOCUS      P046-3-Hli.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
DEFINITION      genomic survey sequence.
ACCESSION      CG752100
VERSION      CG752100.1 GI:37975230
KEYWORDS      GSS.
SOURCE      Pristionchus pacificus
ORGANISM      Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1141)
REFERENCE      Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
AUTHORS      Buntjer,J., van der Meulen,M. and Sommer,R.U.
TITLE      An integrated physical and genetic map of the nematode Pristionchus
JOURNAL      pacificus
PUBMED      Mol. Genet. Genomics 269 (5), 715-722 (2003)
COMMENT      Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1. .1141
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match      83.6%; Score 18.4; DB 10; Length 1141;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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[illegible][illegible]

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/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OC_Ba"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

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Query Match      80.9%; Score 17.8; DB 10; Length 670;
Best Local Similarity 90.5%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGAC 21
    |||||
Db 363 ACAGATAACGTTGCCGGTCAC 383

RESULT 8
CC850938
LOCUS
DEFINITION NDL.10902.T7 Notre Dame Liverpool Aedes aegypti genomic clone
ACCESSION CC850938
VERSION CC850938.1 GI:33202340
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Culicini; Aedes; Stegomyia.
REFERENCE 1 (bases 1 to 969)
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.10902.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .969
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone_lib="Notre Dame Liverpool-10902"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN
Query Match      80.9%; Score 17.8; DB 9; Length 969;
Best Local Similarity 90.5%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGATAACGTTGCCGGTGACG 22
    |||||
Db 495 CCGATAACGTTGCCGGCCACG 515

RESULT 9
DN693955
LOCUS
DEFINITION DN693955 1202 bp mRNA linear EST 30-MAR-2005
CGX91-D12.xid-t SHGC-CGX Gasterosteus aculeatus cDNA clone
CGX91-D12 3', mRNA sequence.
ACCESSION DN693955

```

```

DN693955.1 GI:62050787
EST
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1202)
Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgsc.stanford.edu
Plate: 91
High quality sequence start: 17
High quality sequence stop: 568.
Location/Qualifiers
1. .1202
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CGX91-D12"
/sex="mixed male and female"
/tissue_type="eyes"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCCTAGTCGAGCGCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

ORIGIN
Query Match      80.9%; Score 17.8; DB 8; Length 1202;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGATAACGTTGCCGGTGACG 22
    |||||
Db 344 CCGATGACGCTGCCGGTGACG 364

RESULT 10
CD847930
LOCUS
DEFINITION CD847930 203 bp mRNA linear EST 11-JUL-2003
DH0AB672C09RM1 HaDevR1 Helianthus annuus cDNA clone HaDevR167C09,
mRNA sequence.
ACCESSION CD847930
VERSION CD847930.1 GI:32531752

```



```

KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 203)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..203
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="psc8"
/db_xref="taxon:4232"
/clone="HaDevR167C09"
/tissue_type="leaves"
/clone_lib="HaDevR1"

ORIGIN
Query Match 79.1%; Score 17.4; DB 6; Length 203;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCGATAACGTTCCCGGTGA 20
|||||
Db 67 CCGATAACGTCGCCGTGA 85

RESULT 11
LOCUS CD852670 266 bp mRNA linear EST 11-JUL-2003
DEFINITION DH0ALL82A12Z2M1 HaDevR5 Helianthus annuus cDNA clone HaDevR58A12,
mRNA sequence.
ACCESSION CD852670
VERSION CD852670.1 GI:32536486
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 266)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..266
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="psc8"
/db_xref="taxon:4232"
/clone="HaDevR58A12"
/tissue_type="4 days after self-pollination embryo"

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ORIGIN
Query Match 79.1%; Score 17.4; DB 6; Length 266;
Best Local Similarity 94.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/clone_lib="HaDevR5"

Qy 2 CCGATAACGTTCCCGGTGA 20
|||||
Db 85 CCGATAACGTCGCCGTGA 103

RESULT 12
LOCUS CW511638 334 bp DNA linear GSS 06-OCT-2004
DEFINITION Shotgun_P16_050.b1 Ta004 Triticum aestivum Shotgun Triticum
aestivum genomic, genomic survey sequence.
ACCESSION CW511638
VERSION CW511638.1 GI:53841144
KEYWORDS GSS.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 334)
AUTHORS Gao, W. and Bennetzen, J.L.
TITLE Shotgun sequence analysis of the wheat genome
JOURNAL Unpublished (2004)
COMMENT Contact: Bennetzen JL
Department of Genetics
University of Georgia
1057 Green Street, Athens, GA 30602, USA
Tel: 706 542 9729
Fax: 706 583 0972
Email: maize@uga.edu
Class: shotgun.
Location/Qualifiers
1..334
/organism="Triticum aestivum"
/mol_type="genomic DNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum Shotgun"
/notes="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic
DNA was sheared and the 1-2 kb fragments were cloned into
PCR4-TOPO vector"

FEATURES
source
location/Qualifiers
1..334
/organism="Triticum aestivum"
/mol_type="genomic DNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum Shotgun"
/notes="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic
DNA was sheared and the 1-2 kb fragments were cloned into
PCR4-TOPO vector"

ORIGIN
Query Match 79.1%; Score 17.4; DB 10; Length 334;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GATAACGTTCCCGGTGACG 22
|||||
Db 29 GATTACGTTCCCGGTGACG 47

RESULT 13
LOCUS CW511977 341 bp DNA linear GSS 06-OCT-2004
DEFINITION Shotgun_P16_050.g1 Ta004 Triticum aestivum Shotgun Triticum
aestivum genomic, genomic survey sequence.
ACCESSION CW511977
VERSION CW511977.1 GI:53841483
KEYWORDS GSS.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 341)
AUTHORS Gao, W. and Bennetzen, J.L.

```

TITLE Shotgun sequence analysis of the wheat genome
JOURNAL Unpublished (2004)
COMMENT Contact: Bennetzen JL
Department of Genetics
University of Georgia
1057 Green Street, Athens, GA 30602, USA
Tel: 706 542 9729
Fax: 706 583 0972
Email: maize@uga.edu
Class: shotgun.

FEATURES
source

Location/Qualifiers
1. .341
/organism="Triticum aestivum"
/mol_type="genomic DNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum Shotgun"
/note="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic DNA was sheared and the 1-2 kb fragments were cloned into PCR4-TOPO vector"

ORIGIN

Query Match 79.1%; Score 17.4; DB 10; Length 341;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GATAACGTTGCCGGTGACG 22

Db 306 GATTACGTTGCCGGTGACG 288

RESULT 14

BE523578

LOCUS M38H3 5', mRNA sequence.

DEFINITION BE523578 Arabidopsis developing seed Arabidopsis thaliana cDNA

ACCESSION BE523578

VERSION BE523578.1 GI:9781556

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 384)

AUTHORS White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.

TITLE A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil

JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)

PUBMED 11115876

COMMENT Contact: Benning, C

Dept. of Biochemistry & Molecular Biology

Michigan State University

224 Biochemistry, Michigan State University, East Lansing, MI

48824, USA

Tel: 517 355 1609

Fax: 517 353 9334

Email: benning@msu.edu

Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.

FEATURES
source

Location/Qualifiers
1. .384
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="M38H3"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"

/clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: ECORI; Site_2: XhoII"

ORIGIN

Query Match 79.1%; Score 17.4; DB 2; Length 384;
Best Local Similarity 94.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GATAACGTTGCCGGTGACG 22

Db 327 GATAGCGTTGCCGGTGACG 345

RESULT 15

BP825967

LOCUS BP825967

DEFINITION BP825967 RAFL19 Arabidopsis thaliana cDNA clone RAFL22-70-F16 5', mRNA sequence.

ACCESSION BP825967

VERSION BP825967.1 GI:59879153

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 387)

AUTHORS Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S., Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and Shinozaki, K.

TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs

JOURNAL Unpublished (2005)

COMMENT Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msekic@rctc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously [Seki et al., 1998, 2002]. This clone is in a modified pBluescript vector.

Please visit our web site (<http://pfweb.gsc.riken.jp>) and <http://range.gsc.riken.jp> for further details.

Location/Qualifiers

1. .387

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="RAFL22-70-F16"

/tissue_type="mixture of silique and flower"

/lab_host="DH10B"

/clone_lib="RAFL19"

/note="Site_1: BamHI; Site_2: SalI; Subtraction Library"

ORIGIN

Query Match 79.1%; Score 17.4; DB 3; Length 387;
Best Local Similarity 94.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GATAACGTTGCCGGTGACG 22

Db 324 GATAGCGTTGCCGGTGACG 342

Search completed: May 4, 2006, 07:17:52

Job time : 1563.34 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	18.8	85.5	30	3	US-09-690-921-3	Sequence 3, Appli
2	18.8	85.5	30	3	US-09-301-829A-3	Sequence 3, Appli
3	18.8	85.5	30	3	US-09-672-126B-164	Sequence 164, App
4	18.8	85.5	45	3	US-09-672-126B-163	Sequence 163, App
5	18.8	85.5	268	2	US-08-105-168B-1	Sequence 1, Appli
6	18.8	85.5	268	2	US-08-105-168B-2	Sequence 2, Appli
7	18.8	85.5	268	2	US-08-105-168B-5	Sequence 5, Appli
8	18.8	85.5	268	2	US-08-698-948-1	Sequence 1, Appli
9	18.8	85.5	268	2	US-08-698-948-2	Sequence 2, Appli
10	18.8	85.5	268	2	US-08-698-948-5	Sequence 5, Appli
11	18.8	85.5	314	2	US-08-105-168B-23	Sequence 23, Appl
12	18.8	85.5	314	2	US-08-698-948-23	Sequence 23, Appl
13	18.8	85.5	342	2	US-08-473-020A-31	Sequence 31, Appl
14	18.8	85.5	343	2	US-08-473-020A-4	Sequence 4, Appli
15	18.8	85.5	350	2	US-08-105-168B-22	Sequence 22, Appl
16	18.8	85.5	350	2	US-08-698-948-22	Sequence 22, Appl
17	18.8	85.5	888	3	US-09-613-303-32	Sequence 32, Appl
18	18.8	85.5	888	3	US-10-267-311-32	Sequence 32, Appl
19	18.8	85.5	1623	3	US-09-613-303-3	Sequence 3, Appli
20	18.8	85.5	1623	3	US-10-267-311-3	Sequence 3, Appli
21	18.8	85.5	1623	3	US-09-712-363-23	Sequence 23, Appl
22	18.8	85.5	1920	3	US-09-613-303-16	Sequence 16, Appl
23	18.8	85.5	1920	3	US-10-267-311-16	Sequence 16, Appl
24	18.8	85.5	1947	3	US-09-613-303-28	Sequence 28, Appl

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; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 30
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising
; OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-3

Query Match      85.5%; Score 18.8; DB 3; Length 30;
Best Local Similarity 90.9%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
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Db 1 ACCGATGACGTCCCGGTGACG 22

RESULT 3
US-09-672-126B-164
; Sequence 164, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 164
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-164

Query Match      85.5%; Score 18.8; DB 3; Length 30;
Best Local Similarity 90.9%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
   ||||| ||||| ||||| |||||
Db 1 ACCGATGACGTCCCGGTGACG 22

RESULT 4
US-09-672-126B-163
; Sequence 163, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
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; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-163

Query Match      85.5%; Score 18.8; DB 3; Length 45;
Best Local Similarity 90.9%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
   ||||| ||||| ||||| |||||
Db 1 ACCGATGACGTCCCGGTGACG 22

RESULT 5
US-08-105-168B-1
; Sequence 1, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION OF MYCOBACTERIA
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium bovis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-1
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Query Match 85.5%; Score 18.8; DB 2; Length 268;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
29 ACCGATGACGTCCCGGTGACG 50

Db

RESULT 6
US-08-105-168B-2
; Sequence 2, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium microti
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-2

Query Match 85.5%; Score 18.8; DB 2; Length 268;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22

Db

RESULT 7
US-08-105-168B-5
; Sequence 5, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 bases
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-5

Query Match 85.5%; Score 18.8; DB 2; Length 268;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22

Db

RESULT 8
US-08-698-948-1

||||| 29 ACCGATGACGTCCCGGTGACG 50

Db

RESULT 7
US-08-105-168B-5
; Sequence 5, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 bases
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-5

Query Match 85.5%; Score 18.8; DB 2; Length 268;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22

Db

RESULT 8
US-08-698-948-1

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; Sequence 1, Application US/08698948
; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,168
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835A
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium bovis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-698-948-1
;
; Query Match 85.5%; Score 18.8; DB 2; Length 268;
; Best Local Similarity 90.9%; Pred. No. 9.7;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 ACCGATAACGTTCCCGTGACG 22
; Db 29 ACCGATGACGTCGCCGTGACG 50
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; RESULT 9
; US-08-698-948-2
; Sequence 2, Application US/08698948
; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,168
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835A
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium microti
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-698-948-2
;
; Query Match 85.5%; Score 18.8; DB 2; Length 268;
; Best Local Similarity 90.9%; Pred. No. 9.7;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; QY 1 ACCGATAACGTTCCCGTGACG 22
; Db 29 ACCGATGACGTCGCCGTGACG 50
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; RESULT 10
; US-08-698-948-5
; Sequence 5, Application US/08698948
; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET

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; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,168
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835A
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium microti
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-698-948-2
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; Query Match 85.5%; Score 18.8; DB 2; Length 268;
; Best Local Similarity 90.9%; Pred. No. 9.7;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; QY 1 ACCGATAACGTTCCCGTGACG 22
; Db 29 ACCGATGACGTCGCCGTGACG 50
;
; RESULT 10
; US-08-698-948-5
; Sequence 5, Application US/08698948
; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET

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TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948
FILING DATE: August 16, 1996
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 bases
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 461-728
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-5
Query Match 85.5%; Score 18.8; DB 2; Length 268;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
Db 29 ACCGACGACGTTGCCGGTGACG 50
RESULT 11
US-08-105-168B-23
Sequence 23, Application US/08105168B
Patent No. 5589585
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: August 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 438-751
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-105-168B-23
Query Match 85.5%; Score 18.8; DB 2; Length 314;
Best Local Similarity 90.9%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGGTGACG 22
Db 52 ACCGATGACGTCGCCGGTGACG 73
RESULT 12
US-08-698-948-23
Sequence 23, Application US/08698948
Patent No. 5849901
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:

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/ MEDIUM TYPE: 3.5" DS/HD
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: MS DOS 3.1
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/698,948
/ FILING DATE: August 16, 1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/105,168
/ FILING DATE: August 12, 1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR9210094
/ FILING DATE: August 8, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: William P. Berridge
/ REGISTRATION NUMBER: 30,024
/ REFERENCE/DOCKET NUMBER: WPB 28835A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6400
/ TELEFAX: (703) 836-2787
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 314 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single-stranded
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL:
/ ANTI-SENSE:
/ ORIGINAL SOURCE:
/ ORGANISM: Mycobacterium tuberculosis
/ STRAIN:
/ INDIVIDUAL ISOLATE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ FEATURE:
/ NAME/KEY:
/ LOCATION: 438-751
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION:
/
/ US-08-698-948-23
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/ Query Match 85.5%; Score 18.8; DB 2; Length 314;
/ Best Local Similarity 90.9%; Pred. No. 9.8;
/ Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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/ QY 1 ACCGATAACGTTCCCGTGACG 22
/ Db 52 ACCGATGACGTCGCCGTGACG 73
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/ RESULT 13
/ US-08-473-020A-31
/ Sequence 31, Application US/08473020A
/ Patent No. 5877273
/ GENERAL INFORMATION:
/ APPLICANT: Hance, Allan J
/ APPLICANT: Grandchamp-Desraux, Bernard
/ APPLICANT: Levy-Prebault, Veronique
/ APPLICANT: Gicquel, Brigitte
/ TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
/ applications to the synthesis or detection of nucleic
/ acids, products of expression of such sequences and
/ application as immunogenic compositions.
/ TITLE OF INVENTION: acids, products of expression of such sequences and
/ application as immunogenic compositions.
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Walter H. Dreger
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: U.S.A.
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/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/473,020A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/623,729
/ FILING DATE: 14-DEC-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreger, Walter H
/ REGISTRATION NUMBER: 24190
/ REFERENCE/DOCKET NUMBER: A54435
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 342 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
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/ US-08-473-020A-31
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/ Query Match 85.5%; Score 18.8; DB 2; Length 342;
/ Best Local Similarity 90.9%; Pred. No. 9.9;
/ Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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/ QY 1 ACCGATAACGTTCCCGTGACG 22
/ Db 46 ACCGATGACGTCGCCGTGACG 67
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/ RESULT 14
/ US-08-473-020A-4
/ Sequence 4, Application US/08473020A
/ Patent No. 5877273
/ GENERAL INFORMATION:
/ APPLICANT: Hance, Allan J
/ APPLICANT: Grandchamp-Desraux, Bernard
/ APPLICANT: Levy-Prebault, Veronique
/ APPLICANT: Gicquel, Brigitte
/ TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
/ applications to the synthesis or detection of nucleic
/ acids, products of expression of such sequences and
/ application as immunogenic compositions.
/ TITLE OF INVENTION: acids, products of expression of such sequences and
/ application as immunogenic compositions.
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Walter H. Dreger
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/473,020A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/623,729
/ FILING DATE: 14-DEC-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreger, Walter H
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; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-020A-4

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Best Local Similarity 90.9%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
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DB 47 ACCGATGACGTCGCCGGTGACG 68

RESULT 15

US-08-105-168B-22
; Sequence 22, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:

; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 438-787
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-22

Query Match 85.5%; Score 18.8; DB 2; Length 350;
Best Local Similarity 90.9%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 52 ACCGATGACGTCGCCGGTGACG 73

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 07:24:16 ; Search time 328.736 Seconds
(without alignments)
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Title: US-10-789-758A-3

Perfect score: 22

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications_NA_Main:

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	30	5	US-10-011-635A-5
3	22	100.0	30	6	US-10-304-616-3
4	22	100.0	30	9	US-10-496-501A-3
5	18.8	85.5	30	5	US-10-011-635A-4
6	18.8	85.5	30	5	US-10-011-635A-6
7	18.8	85.5	30	6	US-10-304-616-4
8	18.8	85.5	30	6	US-10-379-164-3
9	18.8	85.5	30	6	US-10-233-902-7
10	18.8	85.5	30	7	US-10-399-356-3
11	18.8	85.5	30	7	US-10-333-448-3
12	18.8	85.5	30	8	US-10-478-188-3
13	18.8	85.5	30	8	US-10-899-771-26
14	18.8	85.5	30	9	US-10-894-655-4
15	18.8	85.5	30	10	US-11-056-463-164
16	18.8	85.5	30	10	US-11-041-636-7
17	18.8	85.5	30	10	US-11-017-103-3
18	18.8	85.5	45	10	US-11-056-463-163
19	18.8	85.5	54	8	US-10-789-758-7
20	18.8	85.5	604	8	US-10-500-586-2
21	18.8	85.5	604	8	US-10-500-586-6
22	18.8	85.5	604	8	US-10-500-586-7
23	18.8	85.5	604	8	US-10-500-586-12

24	18.8	85.5	604	8	US-10-500-586-45	Sequence 45, Appl
25	18.8	85.5	888	5	US-10-267-311-32	Sequence 32, Appl
26	18.8	85.5	888	9	US-10-679-956-32	Sequence 32, Appl
27	18.8	85.5	1620	7	US-10-282-122A-26142	Sequence 26142, A
28	18.8	85.5	1623	3	US-09-712-363-23	Sequence 23, Appl
29	18.8	85.5	1623	5	US-10-267-311-3	Sequence 3, Appl
30	18.8	85.5	1623	7	US-10-282-122A-28196	Sequence 28196, A
31	18.8	85.5	1623	9	US-10-679-956-3	Sequence 3, Appl
32	18.8	85.5	1761	8	US-10-635-211-1	Sequence 1, Appl
33	18.8	85.5	1920	5	US-10-267-311-16	Sequence 16, Appl
34	18.8	85.5	1920	9	US-10-679-956-16	Sequence 16, Appl
35	18.8	85.5	1947	5	US-10-267-311-28	Sequence 28, Appl
36	18.8	85.5	1947	9	US-10-679-956-28	Sequence 28, Appl
37	18.8	85.5	2073	5	US-10-068-059-9	Sequence 9, Appl
38	18.8	85.5	2073	9	US-10-941-049-9	Sequence 9, Appl
39	18.8	85.5	2130	5	US-10-068-059-7	Sequence 7, Appl
40	18.8	85.5	2130	9	US-10-941-049-7	Sequence 7, Appl
41	18.8	85.5	2175	5	US-10-068-059-11	Sequence 11, Appl
42	18.8	85.5	2175	9	US-10-941-049-11	Sequence 11, Appl
43	18.8	85.5	2241	5	US-10-068-059-5	Sequence 5, Appl
44	18.8	85.5	2241	9	US-10-941-049-5	Sequence 5, Appl
45	18.8	85.5	2847	5	US-10-267-311-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-789-758-3
; Sequence 3, Application US/10789758
; Publication No. US20050002958A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Joe
; APPLICANT: Garcon, Nathalie
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45187
; CURRENT APPLICATION NUMBER: US/10/789,758
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/018,704
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/EP00/05841
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: GB 9915204.3
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing a CpG motif
US-10-789-758-3
Query Match 100.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred.No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATAACGTTGCCGTGACG 22
Db 1 ACCGATAACGTTGCCGTGACG 22
RESULT 2
US-10-011-635A-5
; Sequence 5, Application US/10011635A
; Publication No. US20030003579A1
; GENERAL INFORMATION:
; APPLICANT: Kadowaki, No. US20030003579A1limitsu
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: Dendritic cells; Methods
; FILE REFERENCE: DX01206

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; CURRENT APPLICATION NUMBER: US/10/011,635A
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/243,232
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
; NAME/KEY: misc feature
; LOCATION: (1)..(30)
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
US-10-011-635A-5

Query Match      100.0%; Score 22; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 3
US-10-304-616-3
; Sequence 3, Application US/10304616
; Publication No. US20030138413A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation
; TITLE OF INVENTION: METHODS FOR TREATING CANCER
; FILE REFERENCE: SF01482
; CURRENT APPLICATION NUMBER: US/10/304,616
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-304-616-3

Query Match      100.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 4
US-10-496-501A-3
; Sequence 3, Application US/10496501A
; Publication No. US20050235372A1
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: TOMIZAWA, HIDEYUKI
; APPLICANT: YAMAOKA, TAKASHI
; TITLE OF INVENTION: NONHUMAN ANIMAL UNRESPONSIVE TO IMMUNOPOTENTIATING SYNTHETIC
; FILE REFERENCE: 024918-0116
; CURRENT APPLICATION NUMBER: US/10/496,501A
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: PCT/JP02/12234
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: JP 2001-358295
; PRIOR FILING DATE: 2001-11-22
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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide AAC-30
US-10-496-501A-3

Query Match      100.0%; Score 22; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 5
US-10-011-635A-4
; Sequence 4, Application US/10011635A
; Publication No. US20030003579A1
; GENERAL INFORMATION:
; APPLICANT: Kadowaki, No. US20030003579A1imitsu
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: Dendritic cells; Methods
; FILE REFERENCE: DX01206
; CURRENT APPLICATION NUMBER: US/10/011,635A
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/243,232
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
; NAME/KEY: misc feature
; LOCATION: (1)..(30)
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
US-10-011-635A-4

Query Match      85.5%; Score 18.8; DB 5; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 6
US-10-011-635A-6
; Sequence 6, Application US/10011635A
; Publication No. US20030003579A1
; GENERAL INFORMATION:
; APPLICANT: Kadowaki, No. US20030003579A1imitsu
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: Dendritic cells; Methods
; FILE REFERENCE: DX01206
; CURRENT APPLICATION NUMBER: US/10/011,635A
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/243,232
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
; NAME/KEY: misc.feature
; LOCATION: (1)..(30)
; OTHER INFORMATION: Yamamoto, et al. (1994) Jpn. J. Cancer Res. 85:775-779.
US-10-011-635A-6

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```

Query Match      85.5%; Score 18.8; DB 5; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ACCGATAACGTTGCCCGTGACG 22
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DB 1 ACCGATGACGTCGCCGGTGACG 22

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RESULT 7
US-10-304-616-4
; Sequence 4, Application US/10304616
; Publication No. US20030138413A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation
; TITLE OF INVENTION: METHODS FOR TREATING CANCER
; FILE REFERENCE: SF01482
; CURRENT APPLICATION NUMBER: US/10/304,616
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 30
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-304-616-4

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Query Match      85.5%; Score 18.8; DB 6; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ACCGATAACGTTGCCCGTGACG 22
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DB 1 ACCGATGACGTCGCCGGTGACG 22

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RESULT 8
US-10-379-164-3
; Sequence 3, Application US/10379164
; Publication No. US20030161834A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Garcon, Nathalie
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: B45181-1D1
; CURRENT APPLICATION NUMBER: US/10/379,164
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/690,921
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/02920
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/301,829
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: GB 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30

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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-379-164-3

Query Match      85.5%; Score 18.8; DB 6; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCCGTGACG 22
    ||||| ||||| ||||| |||||
DB 1 ACCGATGACGTCGCCGGTGACG 22

RESULT 9
US-10-233-902-7
; Sequence 7, Application US/10233902
; Publication No. US20030194391A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355US
; CURRENT APPLICATION NUMBER: US/10/233,902
; CURRENT FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-233-902-7

```

```

Query Match      85.5%; Score 18.8; DB 6; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ACCGATAACGTTGCCCGTGACG 22
    ||||| ||||| ||||| |||||
DB 1 ACCGATGACGTCGCCGGTGACG 22

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RESULT 10
US-10-399-356-3
; Sequence 3, Application US/10399356
; Publication No. US20040047869A1
; GENERAL INFORMATION:
; APPLICANT: GARCON, NATHALIE
; APPLICANT: CATHERINE MARIE GHISLAINE GERARD
; APPLICANT: JEAN STEPHENNE
; TITLE OF INVENTION: ADJUVANT COMPOSITION COMPRISING AN
; FILE REFERENCE: B45248
; CURRENT APPLICATION NUMBER: US/10/399,356
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: PCT/EP01/11985
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: GB 0025577.8
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotides based on bacterial sequences
; OTHER INFORMATION: comprising dinucleotide CpB repeats
US-10-399-356-3

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Query Match      85.5%; Score 18.8; DB 7; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCCGTGACG 22
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Db 1 ACCGATGACGTCGCCCGTGACG 22

RESULT 11
US-10-333-448-3
; Sequence 3, Application US/10333448
; Publication No. US20040049150A1
; GENERAL INFORMATION:
; APPLICANT: Dalton, Colin Clive
; APPLICANT: Baseman, Richard Lewis
; APPLICANT: Garcon, Nathalie
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: B45229
; CURRENT APPLICATION NUMBER: US/10/333,448
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/08339
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: GB 0017999.4
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligonucleotide
US-10-333-448-3

Query Match      85.5%; Score 18.8; DB 7; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCCGTGACG 22
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Db 1 ACCGATGACGTCGCCCGTGACG 22

RESULT 12
US-10-478-188-3
; Sequence 3, Application US/10478188
; Publication No. US20050019340A1
; GENERAL INFORMATION:
; APPLICANT: GARCON, NATHALIE
; APPLICANT: GERARD, CATHERINE MARIE GHISLAINE
; APPLICANT: STEPHENNE, JEAN
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: B45245
; CURRENT APPLICATION NUMBER: US/10/478,188
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/EP01/11984
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: GB 0025573.7
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: GB 0025574.5
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 09/690,921
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotides based on bacterial sequences
; OTHER INFORMATION: comprising dinucleotide CpG repeats

US-10-478-188-3
Query Match      85.5%; Score 18.8; DB 8; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCCGTGACG 22
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Db 1 ACCGATGACGTCGCCCGTGACG 22

RESULT 13
US-10-899-771-26
; Sequence 26, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-899-771-26

Query Match      85.5%; Score 18.8; DB 8; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCCGTGACG 22
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Db 1 ACCGATGACGTCGCCCGTGACG 22

RESULT 14
US-10-894-655-4
; Sequence 4, Application US/10894655
; Publication No. US20050054601A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Hermann
; APPLICANT: Lipford, Grayson B.
; APPLICANT: Heeg, Klaus
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING A POLYNUCLEOTIDE AND
; TITLE OF INVENTION: OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
; FILE REFERENCE: C1041.70005US02
; CURRENT APPLICATION NUMBER: US/10/894,655
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 09/355,254
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/00367
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
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US-10-894-655-4

Query Match 85.5%; Score 18.8; DB 9; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATACGTTGCCCGTGACG 22
||||| ||||| ||||| |||||
Db 1 ACCGATGACGTCGCCGCGTGACG 22

RESULT 15

US-11-056-463-164
; Sequence 164, Application US/11056463
; Publication No. US2005016988A1
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039.70044US01
; CURRENT APPLICATION NUMBER: US/11/056,463
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 09/672,126
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,147
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 164
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-11-056-463-164

Query Match 85.5%; Score 18.8; DB 10; Length 30;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATACGTTGCCCGTGACG 22
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Db 1 ACCGATGACGTCGCCGCGTGACG 22

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 08:17:52 ; Search time 502.08 Seconds
(without alignments)
178.449 Million cell updates/sec

Title: US-10-789-758A-3

Perfect score: 22

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Searched: 9306428 seqs, 203628586 residues

Total number of hits satisfying chosen parameters: 18612856

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 19: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	30	12	US-10-741-720A-25
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C 4	16.2	73.6	585	7	US-09-925-065A-538356
C 5	16.2	73.6	585	7	US-09-925-065A-538357
6	16.2	73.6	1203	11	US-10-932-182A-947
7	16.2	73.6	1203	11	US-10-932-182A-947
8	16.2	73.6	1247	18	US-11-147-763-1
C 9	16.2	73.6	1428	11	US-10-932-182A-78079
C 10	16.2	73.6	1428	11	US-10-932-182A-78079
11	16.2	73.6	1488	18	US-11-147-763-5
12	16.2	73.6	1812	11	US-10-932-182A-348
13	16.2	73.6	1812	11	US-10-932-182A-348
14	15.8	71.8	25	11	US-10-932-182A-127255

15	15.8	71.8	25	11	US-10-932-182A-127255
16	15.8	71.8	384	11	US-10-932-182A-79319
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18	15.8	71.8	1041	11	US-10-932-182A-82578
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C 20	15.8	71.8	3690	18	US-11-122-396-2
C 21	15.8	71.8	3690	18	US-11-122-396-37
22	15.8	71.8	33260	18	US-11-122-396-1
C 23	15.8	71.8	134499	17	US-11-117-187-192
24	15.6	70.9	25	11	US-10-932-182A-28704
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26	15.6	70.9	25	11	US-10-932-182A-10941
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28	15.6	70.9	180	11	US-10-932-182A-2059
C 29	15.6	70.9	405	11	US-10-932-182A-5807
C 30	15.6	70.9	405	11	US-10-932-182A-5807
31	15.6	70.9	531	7	US-09-925-065A-569677
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33	15.6	70.9	736	17	US-11-212-443-1
34	15.6	70.9	955	18	US-11-096-568A-1495
C 35	15.6	70.9	1180	18	US-11-188-298-171
36	15.6	70.9	1203	18	US-11-079-463-3101
37	15.6	70.9	1317	11	US-10-932-182A-663
38	15.6	70.9	1317	11	US-10-932-182A-663
39	15.6	70.9	1620	18	US-11-232-406A-31
40	15.6	70.9	1776	17	US-11-212-443-3
C 41	15.6	70.9	2028	18	US-11-222-138A-27
42	15.6	70.9	2032	18	US-11-077-619-33
C 43	15.6	70.9	2049	18	US-11-079-463-499
44	15.6	70.9	2916	17	US-11-052-554A-387
45	15.6	70.9	3198	11	US-10-932-182A-3011

ALIGNMENTS

RESULT 1
US-10-741-720A-25
; Sequence 25, Application US/10741720A
; Publication No. US20060058254A1
; GENERAL INFORMATION:
; APPLICANT: DINA, Dino
; APPLICANT: PEARON, Karen L.
; APPLICANT: MARSHALL, Jason
; TITLE OF INVENTION: IMMUNOSTIMULATORY SEQUENCE
; FILE REFERENCE: 377882003300
; CURRENT APPLICATION NUMBER: US/10/741,720A
; PRIOR FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/436,122
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/447,885
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/467,546
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-741-720A-25

Query Match 100.0%; Score 22; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22

Db 1 ACCGATAACGTTGCCGGTGACG 22

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RESULT 2
US-10-741-720A-92
; Sequence 92, Application US/10741720A
; Publication No. US20060058254A1
; GENERAL INFORMATION:
; APPLICANT: DINA, Dino
; APPLICANT: FEARON, Karen L.
; APPLICANT: MARSHALL, Jason
; TITLE OF INVENTION: IMMUNOSTIMULATORY SEQUENCE
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS OF USING THE SAME
; FILE REFERENCE: 377882003300
; CURRENT APPLICATION NUMBER: US/10/741,720A
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/436,122
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/447,885
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; PRIOR APPLICATION NUMBER: US 60/467,546
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-741-720A-92

Query Match 100.0%; Score 22; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATAACGTTGCCGGTGACG 22

RESULT 3
US-10-469-561-7
; Sequence 7, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-7

Query Match 85.5%; Score 18.8; DB 10; Length 30;
Best Local Similarity 90.9%; Pred. No. 0.51;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGACG 22
Db 1 ACCGATACGTCGCCGGTGACG 22

RESULT 4
US-09-925-065A-538356/c
; Sequence 538356, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 538356
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-538356

Query Match 73.6%; Score 16.2; DB 7; Length 585;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGAC 21
Db 304 ACCGATAAAGTTGCGGTTAC 284

RESULT 5
US-09-925-065A-538357/c
; Sequence 538357, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 538357
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-538357

Query Match 73.6%; Score 16.2; DB 7; Length 585;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGAC 21
Db 304 ACCGATAAAGTTGCGGTTAC 284
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RESULT 6
US-10-932-182A-947
; Sequence 947, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 947
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-947

Query Match          73.6%; Score 16.2; DB 11; Length 1203;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGATAACGTTGCCGGTGACG 22
Db 71 CCGATAACGTTTCCGGTGATG 91

RESULT 7
US-10-932-182A-947
; Sequence 947, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 947
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-947

Query Match          73.6%; Score 16.2; DB 11; Length 1203;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGATAACGTTGCCGGTGACG 22
Db 71 CCGATAACGTTTCCGGTGATG 91

RESULT 8
US-11-147-763-1
; Sequence 1, Application US/11147763
; Publication No. US20060078909A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasan, Maichreyan
; APPLICANT: Reifler, Michael
; TITLE OF INVENTION: Sulfurylase-Luciferase Fusion Proteins
; FILE REFERENCE: 21465-504
; CURRENT APPLICATION NUMBER: US/11/147,763
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; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/154,515
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/10/122,706
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/335,949
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1247
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
US-11-147-763-1

Query Match          73.6%; Score 16.2; DB 18; Length 1247;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGATAACGTTGCCGGTGACG 22
Db 235 CCGATCACGCTGGCGGTGACG 255

RESULT 9
US-10-932-182A-78079/c
; Sequence 78079, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78079
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78079

Query Match          73.6%; Score 16.2; DB 11; Length 1428;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACCGATAACGTTGCCGGTGAC 21
Db 1026 ACCGATAACCATGCCAGTGAC 1006

RESULT 10
US-10-932-182A-78079/c
; Sequence 78079, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78079
; LENGTH: 1428
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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127255
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-127255

Query Match 71.8%; Score 15.8; DB 11; Length 25;
Best Local Similarity 89.5%; Pred.No.32;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 3 GATAACGTTACCGGTGAG 21

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:22:43 ; Search time 464.368 Seconds
(without alignments)
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Title: US-10-789-758A-4

Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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13: gb_vi.*
14: gb_hlg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	20	6	BD190419 Microemul
5	20	100.0	20	6	BD251267 Enhanceme
6	20	100.0	20	6	AR182880 Sequence
7	20	100.0	20	6	AR182887 Sequence
8	20	100.0	20	6	AR222213 Sequence
9	20	100.0	20	6	AR432435 Sequence
10	20	100.0	20	6	AR607443 Sequence
11	20	100.0	20	6	AR607450 Sequence
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18	20	100.0	20	6	AX105103 Sequence

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27	20	100.0	20	6	AX547628 Sequence
28	20	100.0	20	6	AX547829 Sequence
29	20	100.0	20	6	AX547830 Sequence
30	20	100.0	20	6	BD009060 Immunosti
31	20	100.0	21	6	AX104812 Sequence
32	20	100.0	21	6	AX105257 Sequence
33	20	100.0	21	6	AX547865 Sequence
34	20	100.0	24	6	AX104326 Sequence
35	20	100.0	24	6	AX547379 Sequence
36	19	95.0	19	6	CQ753472 Sequence
37	19	95.0	19	6	CQ753473 Sequence
38	19	95.0	19	6	CQ888031 Sequence
39	19	95.0	19	6	CQ888032 Sequence
40	19	95.0	19	6	CQ888168 Sequence
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44	19	95.0	19	6	AX771751 Sequence
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ALIGNMENTS

RESULT 1

AR140453

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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AR140453 Sequence 12 from patent US 6207646. linear PAT 16-JUN-2001

AR140453 Sequence 12 from patent US 6207646. linear PAT 16-JUN-2001

AR140453.1 GI:14482949

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg, A.M., Kline, J., Kliman, D. and Steinberg, A.D.

Immunostimulatory nucleic acid molecules

Patent: US 6207646-A 12 27-MAR-2001;

Location/Qualifiers

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/mol_type="unassigned DNA"

100.0%; Score 20; DB 6; Length 20;

100.0%; Pred. No. 26;

0; Mismatches 0; Indels 0; Gaps 0;

0; Indels 0; Gaps 0;

0; Indels 0; Gaps 0;

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0; Indels 0; Gaps 0;

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0; Indels 0; Gaps 0;

RESULT 2

AR154761

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 20)

Krieg, A.M. and Kline, J.N.

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg, A.M. and Kline, J.N.

AR154761 Sequence 90 from patent US 6239116. linear PAT 08-AUG-2001

AR154761 Sequence 90 from patent US 6239116. linear PAT 08-AUG-2001

AR154761.1 GI:15122814

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg, A.M. and Kline, J.N.

Unknown.

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Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 6
LOCUS AR182880 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 52 from patent US 6339068.
ACCESSION AR182880
VERSION AR182880.1 GI:20226087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 52 15-JAN-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 7
LOCUS AR182887 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 59 from patent US 6339068.
ACCESSION AR182887
VERSION AR182887.1 GI:20226094
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 59 15-JAN-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 8
LOCUS AR222213 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 47 from patent US 6429199.
ACCESSION AR222213
VERSION AR222213.1 GI:23329678
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6429199-A 47 23-NOV-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M. and Hartmann,G.
TITLE Immunostimulatory nucleic acid molecules for activating dendritic cells
JOURNAL Patent: US 6429199-A 47 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 9
LOCUS AR432435 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6653292.
ACCESSION AR432435
VERSION AR432435.1 GI:40194770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M. and Weiher,G.
TITLE Method of treating cancer using immunostimulatory oligonucleotides
JOURNAL Patent: US 6653292-A 12 25-NOV-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 10
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DEFINITION Sequence 52 from patent US 6821957.
ACCESSION AR607443
VERSION AR607443.1 GI:56659860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Joachim,S.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6821957-A 52 23-NOV-2004;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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REFERENCE 1
AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE     Immunostimulatory nucleic acids
JOURNAL   Patent: WO 0122972-A 767 05-APR-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
          GmbH (DE)
FEATURES  Location/Qualifiers
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Best Local Similarity 100.0%; Pred. NO. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db  1 GGGGTCAACGTTGAGGGGG 20

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Job time : 467.368 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 4996997 seqs, 332346308 residues

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Maximum Match 100%
Listing first 45 summaries

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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	20	2	AAT16894
5	20	100.0	20	2	AAT16894
6	20	100.0	20	2	AAT16894
7	20	100.0	20	2	AAT16894
8	20	100.0	20	2	AAT16894
9	20	100.0	20	2	AAT16894
10	20	100.0	20	2	AAT16894
11	20	100.0	20	2	AAT16894
12	20	100.0	20	2	AAT16894
13	20	100.0	20	2	AAT16894
14	20	100.0	20	2	AAT16894
15	20	100.0	20	2	AAT16894
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19	20	100.0	20	2	AAT16894

20	20	100.0	20	5	AAF27750	P. falcip
21	20	100.0	20	6	ABS78484	Angiogene
22	20	100.0	20	6	ABS78485	Angiogene
23	20	100.0	20	6	ABS78283	Angiogene
24	20	100.0	20	6	ABS78035	Angiogene
25	20	100.0	20	6	ABL39032	Immunosti
26	20	100.0	20	6	ABL39033	Immunosti
27	20	100.0	20	6	ABK46517	Immunosti
28	20	100.0	20	6	AA144488	CpG motif
29	20	100.0	20	6	ABS70558	Dendritic
30	20	100.0	20	8	ACC48308	CpG oligo
31	20	100.0	20	8	ABZ80163	Immunosti
32	20	100.0	20	9	ACC83113	D class C
33	20	100.0	20	9	ACD99810	Immunosti
34	20	100.0	20	9	ACH03105	Immunosti
35	20	100.0	20	9	ACH03288	Immunosti
36	20	100.0	20	9	ADB37069	Immunosti
37	20	100.0	20	9	ADB37266	Immunosti
38	20	100.0	20	9	ADB36892	Immunosti
39	20	100.0	20	9	ADB37265	Immunosti
40	20	100.0	20	10	ADG60208	Oligonucle
41	20	100.0	20	10	ADG68114	Urmethyla
42	20	100.0	20	12	ADI01054	Immunosti
43	20	100.0	20	12	ACA63219	Toll-like
44	20	100.0	20	12	ADM99023	Immunosti
45	20	100.0	20	12	ADO04739	CpG oligo

ALIGNMENTS

RESULT 1
AAT16894
ID AAT16894 standard; DNA; 20 BP.
XX
AC AAT16894;
XX
DT 06-SEP-1996 (first entry)
XX
DE Immunomodulatory oligonucleotide contg. unmethylated C-G dinucleotide.
XX
KW Unmethylated; immunomodulator; B cell activation; vaccine;
KW response stimulation; autoimmune disease; infection; ss.
XX
OS Synthetic.
PN WO9602555-A1.
XX
PD 01-FEB-1996.
XX
PF 07-FEB-1995; 95WO-US001570.
XX
PR 15-JUL-1994; 94US-00276358.
XX
(IOWA) UNIV IOWA STATE RES FOUND INC.
Krieg AM;
WPI; 1996-105847/11.
Immunomodulatory oligo:nucleotide(s) contg. an un-methylated CpG di-nucleotide - used for stimulating activity or when methylated for inhibitory activity.
Claim 5; Page 39; 45pp; English.
AAT16894-T16898 are immunomodulatory oligonucleotides contg. at least one unmethylated C-G dinucleotide. The oligonucleotides can be used to activate B cells and natural killer cells. They can be used for treating, preventing or ameliorating an immune system deficiency, e.g. a tumour, cancer or a viral, fungal, bacterial or parasitic infection. They are also useful in stimulating a subject's response to a vaccine

```

SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 2
AAV47684
ID AAV47684 standard; DNA; 20 BP.
XX
AC AAV47684;
XX
DT 20-NOV-1998 (first entry)
XX
DE Unmethylated CpG dinucleotide 1585.
XX
KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.
XX
OS Synthetic.
XX
PN WO9837919-A1.
XX
PD 03-SEP-1998.
XX
PF 25-FEB-1998; 98WO-US003678.
XX
PR 28-FEB-1997; 97US-0039405P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Schwartz DA, Krieg AM;
XX
PWPI; 1998-480941/41.
XX
PT Use of nucleic acids containing an unmethylated CpG - for treating a
PT subject having or at risk of having an acute decrement in air flow or
PT inhibiting an inflammatory response.
XX
PS Claim 35; Page 27; 65pp; English.
XX
CC This sequence represents an unmethylated CpG dinucleotide, and can be
CC used in the method of the invention. The method is for treating a subject
CC having, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with Gram-
CC positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC abscesses, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide
XX
SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 4
AAV74238
Db 1 GGGGTCAACGTTGAGGGGG 20
AAV27654
ID AAV27654 standard; DNA; 20 BP.
XX
AC AAV27654;
XX
DT 01-OCT-1998 (first entry)
XX
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
PN WO9818810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US019791.
XX
PR 30-OCT-1996; 96US-00738652.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Kline JN;
XX
PWPI; 1998-272127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at least one
PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
PT or autoimmune disease.
XX
PS Claim 26; Page 83; 109pp; English.
XX
CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC of the invention. The ODNs contain at least one unmethylated CpG
CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
CC thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCG tetramer
CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
CC one nucleotide separates consecutive CpGs, X1 and X2 are selected from
CC GpT, GpG, GpA, ApT and ApA, X3 and X4 are selected from Tpt or Cpt, N is
CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
CC does not contain a CCG tetramer or more than one CCG or CCG trimer. The
CC ODNs activate lymphocytes in a subject and redirect a subject's immune
CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other
CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
CC The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune diseases, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a
CC human
XX
SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 4
AAV74238

```

```

ID  AAV74238 standard; DNA; 20 BP.
XX
AC  AAV74238;
XX
DT  20-MAR-2003 (revised)
DT  15-MAR-1999 (first entry)
XX
DE  CpG-N motif S-ODN 1628 DNA.
XX
XX  CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW  viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW  toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW  hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS  Synthetic.
XX
XX  WO9852581-A1.
XX
XX  26-NOV-1998.
XX
XX  20-MAY-1998; 98WO-US010408.
XX
XX  20-MAY-1997; 97US-0047209P.
XX  20-MAY-1997; 97US-0047233P.
XX
XX  (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
XX  (IOWA) UNIV IOWA RES FOUND.
XX  (QIAG-) QIAGEN GMBH.
XX
XX  Davis HL, Krieg AM, Schorr J, Wu T;
XX  WPI; 1999-059712/05.
XX
XX  Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
XX  enhancing the immunostimulatory effect of an antigen or enhancing the
XX  expression of a therapeutic polypeptide.
XX
XX  Example 1; Page 64; 109pp; English.
XX
XX  AAV74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
XX  method for enhancing the immunostimulatory effect of an antigen encoded
XX  by nucleic acid contained in a nucleic acid construct. The method
XX  involves determining the CpG-N and CpG-S motifs present in the construct,
XX  removing neutralising CpG (CpG-N) motifs and optionally inserting a
XX  stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
XX  nucleic acid construct having enhanced immunostimulatory efficacy. The
XX  method can be used for immunisation against viral antigens, e.g. from
XX  hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
XX  parasite. They can also be used for expression of a therapeutic
XX  polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
XX  apoptotic proteins, interferons, hormones, clotting factors, ligands and
XX  receptors. (Updated on 20-MAR-2003 to correct PA field.)
XX
XX  Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX  Query Match 100.0%; Score 20; DB 2; Length 20;
XX  Best Local Similarity 100.0%; Pred. No. 3;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGGTCAACGTTGAGGGGG 20
DB  1 GGGGTCAACGTTGAGGGGG 20

RESULT 5
AAV74245
ID  AAV74245 standard; DNA; 20 BP.
XX
AC  AAV74245;
XX
DT  20-MAR-2003 (revised)
DT  15-MAR-1999 (first entry)
XX
XX  CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW  viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW  toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW  hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS  Synthetic.
XX
XX  WO9852581-A1.
XX
XX  26-NOV-1998.
XX
XX  20-MAY-1998; 98WO-US010408.
XX
XX  20-MAY-1997; 97US-0047209P.
XX  20-MAY-1997; 97US-0047233P.
XX
XX  (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
XX  (IOWA) UNIV IOWA RES FOUND.
XX  (QIAG-) QIAGEN GMBH.
XX
XX  Davis HL, Krieg AM, Schorr J, Wu T;
XX  WPI; 1999-059712/05.
XX
XX  Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
XX  enhancing the immunostimulatory effect of an antigen or enhancing the
XX  expression of a therapeutic polypeptide.
XX
XX  Example 1; Page 64; 109pp; English.
XX
XX  AAV74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
XX  method for enhancing the immunostimulatory effect of an antigen encoded
XX  by nucleic acid contained in a nucleic acid construct. The method
XX  involves determining the CpG-N and CpG-S motifs present in the construct,
XX  removing neutralising CpG (CpG-N) motifs and optionally inserting a
XX  stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
XX  nucleic acid construct having enhanced immunostimulatory efficacy. The
XX  method can be used for immunisation against viral antigens, e.g. from
XX  hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
XX  parasite. They can also be used for expression of a therapeutic
XX  polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
XX  apoptotic proteins, interferons, hormones, clotting factors, ligands and
XX  receptors. (Updated on 20-MAR-2003 to correct PA field.)
XX
XX  Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX  Query Match 100.0%; Score 20; DB 2; Length 20;
XX  Best Local Similarity 100.0%; Pred. No. 3;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGGTCAACGTTGAGGGGG 20
DB  1 GGGGTCAACGTTGAGGGGG 20

RESULT 6
AAV90449
ID  AAA90449 standard; DNA; 20 BP.
XX
AC  AAA90449;
XX
DT  10-JAN-2001 (first entry)
XX
DE  CpG adjuvant oligonucleotide, SEQ ID NO:3.
XX
XX  CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
KW  microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
KW  viral infection; bacterial infection; parasitic infection; HCV; HBV;
KW  hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
KW  human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
KW  rabies virus; cholera; diphtheria; tetanus; pertussis;

```

KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.
 XX Synthetic.
 OS WO200050006-A2.
 PN 31-AUG-2000.
 PD 09-FEB-2000; 2000WO-US003331.
 PF 26-FEB-1999; 99US-0121858P.
 PR 29-JUL-1999; 99US-0146391P.
 PR 28-OCT-1999; 99US-0161997P.
 XX (CHIR) CHIRON CORP.
 PA O'hagan D, Ott GS, Donnelly J, Kazzaz J, Ugozzoli M, Singh M; Barackman J;
 XX WPI; 2000-587123/55.
 DR Microemulsion having an adsorbent surface comprising a microdroplet emulsion consisting of a metabolizable oil and an emulsifying agent which is a detergent, useful as a vaccine to treat bacterial, viral, and parasitic infection.
 XX Claim 17; Page 40; 95pp; English.
 PS The invention relates to a microdroplet emulsion (microemulsion) with an adsorbent surface, and which comprises a metabolizable oil and an emulsifying agent (a detergent). It also relates to a composition comprising the microemulsion and a microparticle with an adsorbent surface, where the microparticle comprises a polymer selected from a poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polythioester, a polyanhydride, and a polycyanocrylate, and a second detergent. The surface of the microparticles efficiently adsorb biologically active macromolecules such as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes, mediators of transcription or translation, metabolic intermediates and adjuvants. Additionally, a second biologically active molecule may be encapsulated within the microparticle. The microemulsion can be used in methods of immunising a host animal, particularly a human, against a viral, bacterial or parasitic infection, and in methods of increasing a Th1 immune response. The microemulsions (having the appropriate antigens adsorbed) may be particularly used as vaccines for hepatitis C virus (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and rabies virus; the bacteria which cause cholera, diphtheria, tetanus and pertussis; Helicobacter pylori and Haemophilus influenzae; and malaria-causing parasites. Sequences AAA90447-A90467 represent Th1 lymphocyte stimulating oligonucleotides containing at least one CpG motif which are claimed for use as adjuvants in the compositions of the invention
 XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTCAACGTTGAGGGGG 20
 Db 1 GGGGTCAACGTTGAGGGGG 20
 RESULT 7
 AAH20394
 ID AAH20394 standard; DNA; 20 BP.
 AC AAH20394;
 XX
 DT 03-AUG-2001 (first entry)
 XX CpG motif containing oligonucleotide SEQ ID #5.

XX Immune system stimulator; CpG motif; CpG receptor; CpG-R; antibacterial; immune response; vaccine adjuvant; tumour immunotherapy; allergy; anti-inflammatory; cystic fibrosis; sepsis; heart disease; chlamydia; inflammatory bowel disease; arthritis; multiple sclerosis; ss.
 OS Unidentified.
 XX Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod base= OTHER
 /note= "Phosphorothioate internucleoside linkages"
 XX WO200132877-A2.
 XX 10-MAY-2001.
 XX 01-NOV-2000; 2000WO-US041735.
 XX 02-NOV-1999; 99US-0163157P.
 PR 24-NOV-1999; 99US-0167389P.
 XX (CHIR) CHIRON CORP.
 PA Mackichan ML;
 PI WPI; 2001-343486/36.
 DR Novel CpG receptor and nucleic acid molecule encoding the receptor, for modulating immune response and for identifying compounds of therapeutic use which bind and/or modulate the activity of the receptor.
 XX Example 1; Page 14; 41pp; English.
 PS Unmethylated CG dinucleotide sequences are commonly found in bacterial DNA, and have been found to stimulate the innate immune system. Natural killer and T cells are activated by exposure to oligonucleotides containing CpG motifs. Oligonucleotides containing CpG motifs can be used as adjuvants in vaccines. The present invention relates to a CpG receptor. The CpG receptor contains a Toll homology domain (THD). The Toll receptor family are associated with responses to pathogens. CpG oligonucleotides may act as stimulators of various immune responses. The CpG receptor or cells expressing the receptor are useful for identifying a compound which binds to or modulates an activity of the CpG receptor. The compounds are useful in e.g. vaccine adjuvants promoting cell-mediated immune responses, antibacterials, (e.g. protection from Listeria infection), tumour immunotherapy, allergy treatment, (e.g. suppressing IgE in human PBMC, shifting from Th2 to Th1) and as anti-inflammatory agents (e.g. for use in cystic fibrosis, sepsis, heart disease, chlamydia, inflammatory bowel disease, arthritis and multiple sclerosis). The present sequence represents a CpG motif containing oligonucleotide used in examples demonstrating that CpG oligonucleotides can activate the MAPK pathways and NF-kappaB
 XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTCAACGTTGAGGGGG 20
 Db 1 GGGGTCAACGTTGAGGGGG 20
 RESULT 8
 AAH50658
 ID AAH50658 standard; DNA; 20 BP.
 XX AAH50658;
 AC
 XX 22-AUG-2001 (first entry)
 DT


```

XX DE Immune response modulating related oligonucleotide SEQ ID NO:90.
XX KW Immunostimulatory; inducing; natural killer cell; lytic activity;
XX KW unmethylated CpG dinucleotide; immune response; B cell proliferation;
XX KW Th1; immune activation; interleukin 6; IL-6; interferon gamma; IFN-gamma;
XX KW cytokine; ss.
XX OS Synthetic.
XX PN US6239116-B1.
XX PD 29-MAY-2001.
XX PF 30-OCT-1997; 97US-00960774.
XX PR 30-OCT-1996; 96US-00738652.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Krieg AM, Kline JN;
XX DR WPI; 2001-380456/40.
XX PT Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
XX PT natural killer cell lytic activity in a human, comprise administering to
XX PT the subject or exposing a natural killer cell to immunostimulatory
XX PT nucleic acids.
XX PS Disclosure; Col 91; 74pp; English.
XX CC The present invention describes methods for inducing interleukin 6 (IL-
XX CC 6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating natural
XX CC killer cell lytic activity. The methods comprise administering to the
XX CC subject or exposing a natural killer cell to an immunostimulatory nucleic
XX CC acid. Also described are: (1) inducing IL-6 in a subject comprising
XX CC administering to the subject to induce IL-6 in the subject the
XX CC immunostimulatory nucleic acid; (2) stimulating natural killer cell lytic
XX CC activity comprising exposing a natural killer cell to the
XX CC immunostimulatory nucleic acid to stimulate natural killer cell lytic
XX CC activity; (3) inducing interferon-gamma in a subject to treat an immune
XX CC system deficiency comprising administering to the subject to induce
XX CC interferon-gamma production, the immunostimulatory nucleic acid; and (4)
XX CC inducing IL-12 in a subject comprising administering to the subject the
XX CC immunostimulatory nucleic acid. The methods are useful for inducing IL-6,
XX CC interferon-gamma or IL-12, or stimulating natural killer cell lytic
XX CC activity in a subject, particularly a human. The methods are particularly
XX CC useful for modulating an immune response. AAH50571 to AAH50671 represent
XX CC oligonucleotide sequences used in the exemplification of the present
XX CC invention
XX SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
DB 1 GGGGTCAACGTTGAGGGGG 20
|||||
RESULT 9
AAH19262
ID AAH19262 standard; DNA; 20 BP.
XX AC AAH19262;
XX DT 13-JUL-2001 (first entry)
XX DE Oligonucleotide 1585.

```

```

XX KW Immunostimulant; antiallergic; cytostatic; antiasthmatic; vaccine;
XX KW gene therapy; CpG; immune system deficiency; tumour; cancer; infection;
XX KW leukaemia; ss.
XX OS Synthetic.
XX PN US6207646-B1.
XX PD 27-MAR-2001.
XX PF 30-OCT-1996; 96US-00738652.
XX PR 15-JUL-1994; 94US-00276358.
XX PR 07-FEB-1995; 95US-00386063.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Krieg AM, Kline J, Klinman D, Steinberg AD;
XX DR WPI; 2001-280761/29.
XX PT Compositions comprising immunostimulatory molecules which comprise
XX PT unmethylated CpG dinucleotides useful for ameliorating immune system
XX PT deficiency, treating leukemia and desensitizing subject against allergic
XX PT response.
XX PS Example 12; Col 14; 55pp; English.
XX CC The present invention relates to a composition comprising an isolated
XX CC immunostimulatory nucleic acid which comprises unmethylated cytosine-
XX CC guanine (CpG) dinucleotides and an antigen in a carrier. The present
XX CC sequence is an oligonucleotide, which was used in the present invention.
XX CC The immunostimulatory nucleic acids are useful for ameliorating an immune
XX CC system deficiency (the presence of tumour, cancer or infectious agent) in
XX CC a subject. The immunostimulatory nucleic acids are also useful for
XX CC desensitising a subject against the occurrence of an allergic reaction in
XX CC response to contact with a particular allergen. The immunostimulatory
XX CC nucleic acids are also useful for vaccination and for treating leukaemia
XX CC in a subject on administration prior to or in conjunction with a
XX CC chemotherapy, so that the subject's leukaemia cells are more sensitive to
XX CC chemotherapy. The compositions are useful for inducing an antigen
XX CC specific immune response in the subject. The compositions can be also
XX CC used to treat or prevent the symptoms of asthma
XX SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
DB 1 GGGGTCAACGTTGAGGGGG 20
|||||
RESULT 10
AAF98854
ID AAF98854 standard; DNA; 20 BP.
XX AC AAF98854;
XX DT 11-JUN-2001 (first entry)
XX DE Poly-G immunostimulatory nucleic acid SEQ ID NO: 135.
XX KW Immunostimulatory nucleic acid; ISNA; human; interferon alpha; IFN-alpha;
XX KW viral infection; phosphorothioate backbone; palindrome; cancer; ds.
XX OS Synthetic.
XX XX

```


PT Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.

PS Claim 4; Page 37; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC0581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
 |||||
 Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 13

AAF9504

ID AAF9504 standard; DNA; 20 BP.

XX AAF9504;

XX 24-APR-2001 (first entry)

XX Immunostimulatory CpG oligonucleotide WD1004 for use in an HIV vaccine.

XX Immunostimulatory CpG oligonucleotide; adjuvant; HIV antigen;

XX HIV infection; vaccine; prophylaxis; treatment; ss.

XX Synthetic.

XX WO200100232-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-EP005998.
 XX
 XX 29-JUN-1999; 99GB-00015205.
 PR 31-JAN-2000; 2000GB-00002200.
 XX
 XX (SMJK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA Garcon N, Voss G;
 XX WPI; 2001-122974/13.

XX New vaccine formulation comprising human immunodeficiency virus (HIV)
 PT antigen and immunostimulatory CpG oligonucleotide, useful for preventing
 PT and treating HIV infections in a patient.

XX Claim 10; Page 17; 23pp; English.

XX The invention relates to an HIV vaccine comprising an HIV antigen and an
 CC immunostimulatory oligonucleotide (AAF9501-AAF9508). With the exception
 CC of oligonucleotide WD1005 (AAF9505), the immunostimulatory
 CC oligonucleotides contain at least one unmethylated CpG motif. In
 CC preferred embodiments the internucleotide linkage is phosphorodithioate,
 CC although phosphodiester and other internucleotide bonds, or mixtures of
 CC linkages are within the scope of the invention. The HIV antigen may be
 CC selected from gp160, gp120, Nef, Tat, and Nef or Tat derivatives or
 CC fusion proteins. The vaccine is used for the prophylaxis or treatment of
 CC HIV infection in a patient. The present sequence represents a
 CC specifically claimed immunostimulatory CpG oligonucleotide for use in the
 CC vaccine of the invention

XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
 |||||
 Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 14

AAF9567

ID AAF9567 standard; DNA; 20 BP.

XX AAF9567;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #683.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US026383.

XX 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156135P.

PR 23-AUG-2000; 2000US-0227436P.

XX (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

```

XX WPI; 2001-273485/28.
DR Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 53; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20
RESULT 15
AAF99764
ID AAF99764 standard; DNA; 20 BP.
XX
AC AAF99764;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #880.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
DR Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 57; 338pp; English.
XX

```

```

CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGGTCAACGTTGAGGGGG 20
Search completed: May 4, 2006, 02:44:30
Job time : 156.46 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:45:02 ; Search time 1417.59 Seconds
(without alignments)
660.095 Million cell updates/sec

Title: US-10-789-758A-4

Perfect score: 20
Sequence: 1 999gtcaacgttgagg999g 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	92.0	938	10	AG856275 Oryza sat
C 2	18.4	90.0	905	10	CZ950619 265595 To
C 3	17.4	87.0	260	2	BB584327 BB584327
C 4	17.4	87.0	673	5	BW580781 BW580781
C 5	17.4	87.0	708	2	BB629098 BB629098
C 6	17.4	87.0	737	2	BG747032 602704423
C 7	17.4	87.0	868	8	DR735254 FCAS08092
C 8	17.4	87.0	957	5	BU956037 AGENCOURT
C 9	17.4	87.0	1244	2	BE962736 601656126
C 10	17.4	87.0	787	5	EX386891 EX386891
C 11	17.4	87.0	791	9	CC506640 CH240 348
C 12	17.4	87.0	1008	5	BX356727 BX356727
C 13	16.8	84.0	196	6	CA452850 3528_1_10
C 14	16.8	84.0	244	7	CN657439 RC49fil.y
C 15	16.8	84.0	382	5	BY084323 BY084323
C 16	16.8	84.0	393	10	CW790508 SP_Ba006
C 17	16.8	84.0	406	3	BM001652 1031097F0
C 18	16.8	84.0	414	5	BX678404 BX678404
C 19	16.8	84.0	457	5	BY277221 BY277221
C 20	16.8	84.0	468	6	CA577271 K0707A12-
C 21	16.8	84.0	473	7	CO076646 GR_Ea38B
C 22	16.8	84.0	486	6	CF484305 POLI_4_A1

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C 24	16.8	84.0	516	7	CO076740 GR_Ea38D
C 25	16.8	84.0	522	7	CK391782 K0835F09-
C 26	16.8	84.0	532	1	AL830714 AL830714
C 27	16.8	84.0	533	2	BG355722 EM1_18_F0
C 28	16.8	84.0	558	5	BX253788 BX253788
C 29	16.8	84.0	569	7	CF895871 A0203E02-
C 30	16.8	84.0	571	10	CW016402 ZMMBLC000
C 31	16.8	84.0	594	7	CF897160 A0221A07-
C 32	16.8	84.0	595	7	CF896689 A0214B08-
C 33	16.8	84.0	607	5	BQ418485 ik45C07.Y
C 34	16.8	84.0	660	10	CZ083483 OM_Ba008
C 35	16.8	84.0	667	10	CW265478 104_734_1
C 36	16.8	84.0	669	6	CB663538 OSJNEd08K
C 37	16.8	84.0	680	3	BI716183 1031007G0
C 38	16.8	84.0	690	5	BY758462 BY758462
C 39	16.8	84.0	692	9	BZ714778 OGEA161TM
C 40	16.8	84.0	700	2	BF607967 MV1_00090
C 41	16.8	84.0	713	10	CW265479 104_734_1
C 42	16.8	84.0	717	8	CX724308 1331902_N
C 43	16.8	84.0	755	9	AZ099791 RPCI-23-4
C 44	16.8	84.0	763	9	CC927270 t106j14ba
C 45	16.8	84.0	766	9	BZ714768 OGEA161TC

ALIGNMENTS

RESULT 1
AG856275/c

LOCUS
DEFINITION

ACCESSION
AG856275

VERSION
GSS.

KEYWORDS
Oryza sativa (indica cultivar-group)

SOURCE
Oryza sativa (indica cultivar-group)

ORGANISM
Oryza sativa (indica cultivar-group)

REFERENCE
1

AUTHORS
Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,

TITLE
End Sequencing and Chromosomal in silico Mapping of BAC Clones

JOURNAL
Breeding Science 54, 273-279 (2004)

REFERENCE
2 (bases 1 to 938)

AUTHORS
Sasaki, T., Matsumoto, T. and Wu, J.

TITLE
Direct Submission

JOURNAL
Submitted (29-OCT-2004) Takuji Sasaki, National Institute of

AG856275
Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
BAC clone:K0155C03_R, genomic survey sequence.

AG856275.1
GI:55322510

GSS.
Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzoideae; Oryza.

1
Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,

Karayose, Y., Namiki, N., Matsumoto, T. and Sasaki, T.

End Sequencing and Chromosomal in silico Mapping of BAC Clones

Derived from an indica Rice Cultivar, Kasalath

Breeding Science 54, 273-279 (2004)

2 (bases 1 to 938)

Sasaki, T., Matsumoto, T. and Wu, J.

Direct Submission

Submitted (29-OCT-2004) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki, 305-8602, Japan

(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,

Tel: 81-298-38-7441, Fax: 81-298-38-7468)

The orientation of the sequence is from SP6 side of the BAC clone.

Location/Qualifiers

1. .938

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Kasalath"

/db_xref="taxon:39946"

/clone="K0155C03_R"

Query Match 92.0%; Score 18.4; DB 10; Length 938;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTCACGTTGAGGGGG 20

DB 652 GGGGTCACCTTGAGGGGG 633

RESULT 2
 C2950619/c
 LOCUS
 DEFINITION 265595 Tomato EcorI BAC Library Lycopersicon esculentum genomic
 clone SL EcorI0050D17 3, genomic survey sequence.

ACCESSION C2950619
 VERSION 1
 KEYWORDS C2950619.1 GI:72293351
 SOURCE GSS.

ORGANISM Lycopersicon esculentum (Solanum lycopersicon)
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 905)
 AUTHORS Mueller L.A., Buelis R.M., Wang Y., Tanksley S.D., Giovannoni J.J.,
 Van Eck J. and Stack S.

TITLE BAC end sequencing from three Solanum lycopersicon libraries
 JOURNAL Unpublished (2005)

COMMENT Other_GSSs: 261115
 Contact: Lukas Mueller
 Tanksley Lab, Dept. of Plant Breeding
 Cornell University
 251 Emerson Hall, Ithaca, NY 14853, USA
 Tel: 607-255-6557
 Fax: 607-255-6683
 Email: sgn-feedback@sgn.cornell.edu
 Plate: 50 row: D column: 17
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 24
 High quality sequence stop: 751.

FEATURES
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGG 18
 |||||
 Db 331 GGGGTCAACGTTGAGGGG 314

RESULT 3
 BB584327
 LOCUS
 DEFINITION BB584327 RIKEN full-length enriched, adult male epididymis Mus
 musculus cDNA clone 9230105E24 5', mRNA sequence.

ACCESSION BB584327
 VERSION BB584327.1 GI:11480871
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Murinae; Mus.

REFERENCE 1 (bases 1 to 260)
 AUTHORS Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,
 Carninci, P., Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T.,
 Hodojima, Y., Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J.,
 Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y.,
 Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T.,
 Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
 Unpublished (2000)

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S.,
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 Location/Qualifiers
 1..260
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="9230105E24"
 /sex="male"
 /tissue_type="epididymis"
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 /clone_lib="RIKEN full-length enriched, adult male
 epididymis"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 185.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATTCGAGTTAATAATTAATCCCCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
 BamHI"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 2; Length 260;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTCAACGTTGAGGGGG 20
 |||||
 Db 134 GGGTCAACGTTGAGGGGG 152

RESULT 4
 BW580781

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1710 row: n column: 06
 High quality sequence stop: 727.

FEATURES

source

1..737
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4857797"
 /lab_host="PH10B (phage-resistant)"
 /tissue_type="adenocarcinoma cell line"
 /clone_lib="NIH_MGC_15"
 /note="Organ: colon; Vector: pOTB7; Site: 1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 737;
 Best Local Similarity 94.7%; Pred. No. 8.7e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GGGTCAACGTTGAGGGGG 20
 |||||
 Db 666 GGGTCAACTTGAGGGGG 684

RESULT 7

DR735254
 LOCUS DR735254
 DEFINITION FGAS080924 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
 aestivum cDNA, mRNA sequence.
 ACCESSION DR735254
 VERSION DR735254.1 GI:70962058
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 868)

REFERENCE

AUTHORS Allard, F., Crosby, M.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
 Penniket, C., Roach, J.B. and Sarhan, F.
 Functional Genomics of Abiotic Stresses in Wheat and Canola Crops
 Unpublished (2003)
 Contact: Patrick Gulick
 Plant Molecular Biology
 Concordia University, Department of Biology
 7141 Sherbrooke St. West, Montreal, Quebec H4B 1R6, Canada
 Tel: 514 848 2424 Ext 3407
 Fax: 514 848 2881
 Email: pgulicke@cor.concordia.ca
 This sequence is the direct result of the Base calling software

phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [113,915].

Plate: LLC116-3P row: L column: 17.

FEATURES

source

Location/Qualifiers
 1..868
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 3 Gate 6"
 /note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
 control, cold-acclimated and salt stressed wheat cultivar
 Norstar. 7 mRNA populations were combined before
 constructing the library; 7 day non-acclimated roots, 1,
 23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
 hours and 6 hours treated roots with 200mM NaCl.
 Non-acclimated and cold-acclimated plants were grown in
 vermiculite while salt stressed plant were grown
 hydroponically. First strand synthesis in this library was
 done in the presence of methylated dCTP thereby protecting
 from internal cleavage with NotI."

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 868;
 Best Local Similarity 94.7%; Pred. No. 8.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGTCAACGTTGAGGGGG 19
 |||||
 Db 621 GGGGTCAAGTCGAGGGGG 639

RESULT 8

BU956037/c
 LOCUS BU956037
 DEFINITION AGENCOURT 10621227 NIH_MGC 107 Homo sapiens cDNA clone
 IMAGE:6729514 5', mRNA sequence.
 ACCESSION BU956037
 VERSION BU956037.1 GI:24185609
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM3052 row: n column: 09
 High quality sequence stop: 569.

FEATURES

source

Location/Qualifiers
 1..957
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6729514"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 5; Length 957;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGG 19

Db 673 GGGGTCAACGTTGAGGGTG 655

RESULT 9

BE962736/c
LOCUS BE962736 1244 bp mRNA linear EST 14-DEC-2000
DEFINITION 601656126R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855702 3',
mRNA sequence.

ACCESSION BE962736

VERSION BE962736.2 GI:11765940

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 1244)

NIH-MGC <http://mgc.hci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Oct 3, 2000 this sequence version replaced gi:10573441.

Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM570 row: d column: 07

High quality sequence stop: 61.

Location/Qualifiers

FEATURES

1..1244

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3855702"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_66"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 1244;
Best Local Similarity 94.7%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCAACGTTGAGGGG 20

Db 892 GGGTCAACGCTGAGGGGG 874

RESULT 10

BE386891
LOCUS BE386891 787 bp mRNA linear EST 26-APR-2004
DEFINITION 601656126R1 NIH_MGC_66 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens

cDNA clone CS0DB006YB08 3-PRIME, mRNA sequence.

BE386891

VERSION BE386891.2 GI:46571903

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 787)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30447483.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8682.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?cs=CS1DB002D07NP1&c=8682.f>.

Location/Qualifiers

1..787

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DB006YB08"

/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 85.0%; Score 17; DB 5; Length 787;

Best Local Similarity 89.5%; Pred. No. 1.4e+03;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGG 19

Db 126 GGGGTCAACGTTGAGGGG 144

RESULT 11

CC506640/c

LOCUS CC506640

DEFINITION CH240_348M23.T7 CHORI-240 Bos taurus genomic clone CH240_348M23,
genomic survey sequence.

ACCESSION CC506640

VERSION CC506640.1 GI:31824933

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 791)

REFERENCE

AUTHORS

Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barrie, W.,
Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Other GSSs: CH240_348M23.TARBAC13P2

Contact: Rob Holt

Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdj@ngs@mail.choi.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.html>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 348 row: M column: 23
Seq primer: 17
Class: BAC ends.

FEATURES

Location/Qualifiers
1..791
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_348M23"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 791;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTCAACGTTGAGGGG 19

Db 779 GGTCAACGTTGAGGGG 763

RESULT 12
BX356727
LOCUS
DEFINITION
BX356727 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI016YI14 3-PRIME, mRNA sequence.

ACCESSION
BX356727

VERSION
BX356727.2 GI:46304629

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 (bases 1 to 1008)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30374084.

CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8682.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?sc=CSODI016B07NP1&c=8682.f>.

FEATURES

Location/Qualifiers
1..1008

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI016YI14"

/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 85.0%; Score 17; DB 5; Length 1008;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGG 19

Db 111 GGGGTCAACGTTGAGGGG 129

RESULT 13

CA452850

LOCUS

DEFINITION

CA452850

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3528_1_10_1 row: F column: 12.

LOCATION/Qualifiers

1..196

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue type="ear"

/dev stage="0.5 cm - 2.0 cm"

/lab_host="XLOLR"

/clone_lib="3528 - Positive selection of MADS-box genes
from ear library 946"

/note="Organ: immature ear; Vector: pAD-GAL4; Site 1:
EcoRI; Site 2: XhoI; Schmidt lab dissected immature ears
between 0.5 cm - 2.0 cm. Sharon Stanfield prepared the
cDNA library in HybriZAP. Positive selection by probing
with the pooled full-length cDNA of the following MADS box
genes: ZAGL8B, ZAGL9B, ZAGL17, SI, ZAG1, ZAG2, ZAPLA,
ZM2, and ZPIA. Negative selection by probing with pooled
3'-end fragments of the same DNA. The final library is
derived from a total of 210 selected plaques that
hybridized with the full-length cDNA probes, but not with
the 3'-end cDNA probes."

FEATURES

source

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 196;

Best Local Similarity 90.0%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
 ||||| ||||| ||||| |||||
 Db 160 GGGGTCAATCTTGAGGGGG 179

RESULT 14

CN657439/c

LOCUS

DEFINITION Pristionchus pacificus mixed stage SL2b TOPO v1
 Pristionchus pacificus cDNA 5' similar to SW:RLA1_CABEL P91913 60S
 ACIDIC RIBOSOMAL PROTEIN P1. ; mRNA sequence.

ACCESSION

CN657439

VERSION

1 (bases 1 to 244)

KEYWORDS

EST.

SOURCE

Pristionchus pacificus

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

REFERENCE

1 (bases 1 to 244)

AUTHORS

McCartier, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Tsagarisvili, R., Ronko, I., Kennedy, S., McGuire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schur, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

TITLE

Unpublished (1999)

JOURNAL

Contact: McCarter JP

COMMENT

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: es@watson.wustl.edu

Library constructed by: Irina Ronko and Dr. Makedonka Mitreva

Trace considered overall poor quality

Seq primer: SL2b primer

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..244

/organism="Pristionchus pacificus"

/mol_type="mRNA"

/db_xref="taxon:54126"

/dev_stage="Mixed"

/lab_host="DH10B"

/clone_lib="Pristionchus pacificus mixed stage SL2b TOPO

v1"

/note="Vector: pCRII-TOPO (Invitrogen); Site 1: 5': ECORI;

Site 2: 3': ECORI; The library was constructed by Irina

Ronko and Dr. Makedonka Mitreva

(mmitreva@watson.wustl.edu) at Washington University, St.

Louis. Oligo(dT)-SL2b PCR based library. Pristionchus

pacificus mixed stage cDNA PCR products of size >400

nucleotides containing SL2b (GGTTTAAACCCAGTATCTCAAG) on

the 5' end and oligo(dT) on the 3' end were

non-directionally cloned into pCRII-TOPO(Invitrogen)

following the TOPO TA cloning protocol."

ORIGIN

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 7; Length 244;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GGGGTCAACGTTGAGGGGG 20

Db

43 GGGGTCAACGTTGAGGGGG 24

RESULT 15

BY084323/c

LOCUS

DEFINITION

BY084323 RIKEN full-length enriched, 16 days embryo whole body Mus

ACCESSION

BY084323

VERSION

BY084323.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 382)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, K.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gustinich, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltas, L., Marchionni, L., McKenziel, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,

Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wyntshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imosani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation

JOURNAL

of 60,770 full-length cDNAs

PUBMED

Nature 420, 563-573 (2002)

COMMENT

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numasaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

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1..382
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630047M11"
/tissue_type="whole body"
/dev_stage="16 days embryo"
/clone_lib="RIKEN full-length enriched, 16 days embryo
whole Body"
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ORIGIN

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 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20

DB 361 GGGGTCAACGTTGAGGGGG 342

Search completed: May 4, 2006, 07:17:48
 Job time : 1421.59 secs

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		Match	Length			
1	20	100.0	20	3	US-09-888-326-436	Sequence 436, App
2	20	100.0	20	3	US-09-888-326-437	Sequence 437, App
3	20	100.0	20	3	US-09-818-918-12	Sequence 12, App1
4	20	100.0	20	3	US-09-776-479-519	Sequence 519, App
5	20	100.0	20	3	US-09-776-479-517	Sequence 767, App
6	20	100.0	20	3	US-09-776-479-968	Sequence 968, App
7	20	100.0	20	3	US-09-776-479-969	Sequence 969, App
8	20	100.0	20	3	US-09-967-464-3	Sequence 3, App11
9	20	100.0	20	3	US-09-776-479-519	Sequence 519, App
10	20	100.0	20	3	US-09-776-479-767	Sequence 767, App
11	20	100.0	20	3	US-09-776-479-968	Sequence 968, App
12	20	100.0	20	3	US-09-776-479-969	Sequence 969, App
13	20	100.0	20	3	US-09-965-101-52	Sequence 52, App1
14	20	100.0	20	3	US-09-965-101-59	Sequence 59, App1
15	20	100.0	20	5	US-10-112-653-496	Sequence 496, App
16	20	100.0	20	5	US-10-112-653-740	Sequence 740, App
17	20	100.0	20	5	US-10-112-653-923	Sequence 923, App
18	20	100.0	20	5	US-10-017-995-519	Sequence 519, App
19	20	100.0	20	5	US-10-017-995-767	Sequence 767, App
20	20	100.0	20	5	US-10-017-995-968	Sequence 968, App
21	20	100.0	20	5	US-10-017-995-969	Sequence 969, App
22	20	100.0	20	5	US-10-161-229-47	Sequence 47, App1
23	20	100.0	20	6	US-10-194-035-89	Sequence 89, App1

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/ CURRENT APPLICATION NUMBER: US/09/888,326
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: US 60/213,346
/ PRIOR FILING DATE: 2000-06-22
/ NUMBER OF SEQ ID NOS: 848
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 437
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-437
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Db 1 GGGGTCAACGTTGAGGGGG 20
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RESULT 3

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US-09-818-918-12
/ Sequence 12, Application US/09818918
/ Publication No. US20030050261A1
/ GENERAL INFORMATION:
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Kline, Joel N.
/ APPLICANT: Klinman, Dennis
/ APPLICANT: Steinberg, Alfred D.
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
/ FILE REFERENCE: C1039/7048 (AWS)
/ CURRENT APPLICATION NUMBER: US/09/818,918
/ CURRENT FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: US 08/276,358
/ PRIOR FILING DATE: 1994-07-15
/ PRIOR APPLICATION NUMBER: US 08/386,063
/ PRIOR FILING DATE: 1995-02-07
/ PRIOR APPLICATION NUMBER: US 08/738,652
/ PRIOR FILING DATE: 1996-10-30
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 12
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide
US-09-818-918-12
```

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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGGTCAACGTTGAGGGGG 20
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RESULT 4

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US-09-776-479-519
/ Sequence 519, Application US/09776479
/ Publication No. US20030087848A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fouron, Yves
```

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/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ TITLE OF INVENTION: Treatment of Asthma and Allergy
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 519
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-519
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGGTCAACGTTGAGGGGG 20
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RESULT 5

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US-09-776-479-767
/ Sequence 767, Application US/09776479
/ Publication No. US20030087848A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fouron, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ TITLE OF INVENTION: Treatment of Asthma and Allergy
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 767
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-767
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```
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
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   |||||
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RESULT 6

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US-09-776-479-968
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/ Publication No. US20030087848A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fouron, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ TITLE OF INVENTION: Treatment of Asthma and Allergy
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ CURRENT FILING DATE: 2001-02-02
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; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 968
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-968

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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 7

US-09-776-479-969
; Sequence 969, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 969
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-969

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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
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Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 8

US-09-967-464-3
; Sequence 3, Application US/09967464
; Publication No. US20030138453A1
; GENERAL INFORMATION:
; APPLICANT: O'Hagan, Derek
; APPLICANT: Otten, Gillis
; APPLICANT: Donnelly, John J.
; APPLICANT: Polo, John M.
; APPLICANT: Barnett, Susan
; APPLICANT: Singh, Mamohan
; APPLICANT: Dubensky, Jr., Thomas W.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF HETEROLOGOUS NUCLEIC ACIDS
; FILE REFERENCE: PP16269, 004
; CURRENT APPLICATION NUMBER: US/09/967,464
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/236,105

; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/315,905
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence is synthesized
US-09-967-464-3

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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 9

US-09-776-479-519
; Sequence 519, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 519
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-519

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
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Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 10

US-09-776-479-767
; Sequence 767, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0

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; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
; OTHER INFORMATION: in between.
US-09-965-101-59
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
DB      1 GGGGTCAACGTTGAGGGGG 20
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RESULT 15
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; Sequence 496, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Kries, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-496
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
DB      1 GGGGTCAACGTTGAGGGGG 20
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 Job time : 298.851 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 08:17:52 ; Search time 456.437 Seconds
(without alignments)
178.449 Million cell updates/sec

Title: US-10-789-758A-4
Perfect score: 20
Sequence: 1 999gtcaacgttgagg99999 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

Database : Published Applications NA.New.*
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2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
7: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
11: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
12: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3.*
13: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq4.*
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16: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
17: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
18: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq5.*
19: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-10-619-279-12
2	20	100.0	20	10	US-10-435-656-12
3	20	100.0	20	12	US-10-382-822-12
4	20	100.0	20	14	US-11-296-572-12
5	20	100.0	20	17	US-11-127-654-496
6	20	100.0	20	17	US-11-127-654-740
7	20	100.0	20	17	US-11-127-654-923
8	20	100.0	20	17	US-11-134-918-12
9	20	100.0	20	17	US-11-031-460-12
10	20	100.0	20	17	US-11-067-587-12
11	20	100.0	21	17	US-11-127-654-957
12	20	100.0	24	17	US-11-127-654-495
13	18.4	92.0	20	15	US-11-127-797-1
14	18.4	92.0	20	15	US-11-127-803-1

15	18.4	92.0	20	15	US-11-128-127-1	Sequence 1, Appli
16	16.8	84.0	20	17	US-11-127-654-348	Sequence 348, App
17	16.8	84.0	20	17	US-11-127-654-878	Sequence 878, App
18	16.8	84.0	20	17	US-11-127-654-924	Sequence 924, App
19	16.8	84.0	20	17	US-11-127-654-933	Sequence 933, App
20	16.8	84.0	20	17	US-11-127-654-1038	Sequence 1038, Ap
21	16.8	84.0	20	17	US-11-127-654-1040	Sequence 1040, Ap
22	16.8	84.0	21	17	US-11-127-654-908	Sequence 908, App
23	16.8	84.0	21	17	US-11-127-654-915	Sequence 915, App
24	16.8	84.0	21	17	US-11-127-654-956	Sequence 956, App
25	16.8	84.0	655	7	US-09-925-065A-592670	Sequence 592670,
26	16.8	84.0	4224	17	US-11-136-537-2386	Sequence 2386, Ap
27	16.4	82.0	2091	10	US-10-955-054A-37	Sequence 37, Appl
28	16	80.0	20	17	US-11-127-654-475	Sequence 475, App
29	15.8	79.0	19	17	US-11-127-654-930	Sequence 930, App
30	15.8	79.0	19	17	US-11-127-654-931	Sequence 931, App
31	15.8	79.0	603	7	US-09-925-065A-531288	Sequence 531288,
32	15.8	79.0	656	7	US-09-925-065A-785514	Sequence 785514,
33	15.8	79.0	656	7	US-09-925-065A-845021	Sequence 845021,
34	15.8	79.0	951	12	US-10-301-480-598131	Sequence 598131,
35	15.8	79.0	951	12	US-10-301-480-1211540	Sequence 1211540,
36	15.8	79.0	2004	18	US-11-072-512-1222	Sequence 1222, Ap
37	15.4	77.0	19	10	US-10-497-591A-103	Sequence 103, App
38	15.4	77.0	607	7	US-09-925-065A-414201	Sequence 414201,
39	15.4	77.0	615	12	US-10-301-480-480078	Sequence 480078,
40	15.4	77.0	615	12	US-10-301-480-1093487	Sequence 1093487,
41	15.4	77.0	3387	11	US-10-932-182A-1894	Sequence 1894, Ap
42	15.4	77.0	3387	11	US-10-932-182A-1894	Sequence 1894, Ap
43	15.2	76.0	20	10	US-10-435-656-50	Sequence 50, Appl
44	15.2	76.0	20	12	US-10-382-822-41	Sequence 41, Appl
45	15.2	76.0	20	14	US-11-296-572-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-619-279-12
; Sequence 12, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-12

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 2
US-10-435-656-12
; Sequence 12, Application US/10435656
; Publication No. US2005027604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-12

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGGG 20

RESULT 3
US-10-382-822-12
; Sequence 12, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; FILE REFERENCE: C01039.70062.US
; CURRENT APPLICATION NUMBER: US/10/382,822
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-382-822-12

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTCAACGTTGAGGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGGG 20

RESULT 4
US-11-296-572-12
; Sequence 12, Application US/11296572
; Publication No. US20060089326A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/296,572
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-296-572-12

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGGG 20

RESULT 5
US-11-127-654-496
; Sequence 496, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 496
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-496

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
DB 1 GGGGTCAACGTTGAGGGGG 20

RESULT 6

US-11-127-654-740
; Sequence 740, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 740
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-740

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
DB 1 GGGGTCAACGTTGAGGGGG 20

RESULT 7

US-11-127-654-923
; Sequence 923, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 923
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-923

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
DB 1 GGGGTCAACGTTGAGGGGG 20

RESULT 8

US-11-134-918-12
; Sequence 12, Application US/11134918
; Publication No. US20050267064A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/134,918
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-134-918-12

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
DB 1 GGGGTCAACGTTGAGGGGG 20

RESULT 9

US-11-031-460-12
; Sequence 12, Application US/11031460
; Publication No. US20050277609A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/031,460
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-11-031-460-12

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-031-460-12

Query Match          100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 10
US-11-067-587-12
; Sequence 12, Application US/11067587
; Publication No. US20060003955A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/067,587
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-067-587-12

Query Match          100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 11
US-11-127-654-957
; Sequence 957, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 957
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-957

Query Match          100.0%; Score 20; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 2 GGGGTCAACGTTGAGGGGG 21

RESULT 12
US-11-127-654-495
; Sequence 495, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 495
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-495

Query Match          100.0%; Score 20; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 5 GGGGTCAACGTTGAGGGGG 24

RESULT 13
US-11-127-797-1
; Sequence 1, Application US/11127797
; Publication No. US20050245477A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/11/127,797
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/10/690,495
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-797-1
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; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-797-1

Query Match 92.0%; Score 18.4; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.9;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTTCAGGGGG 20

RESULT 14

US-11-127-803-1
; Sequence 1, Application US/11127803
; Publication No. US20050244379A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/11/127,803
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/10/690,495
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-803-1

Query Match 92.0%; Score 18.4; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.9;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTTCAGGGGG 20

RESULT 15

US-11-128-127-1
; Sequence 1, Application US/11128127
; Publication No. US20050244380A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/11/128,127
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/10/690,495
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-128-127-1

Query Match 92.0%; Score 18.4; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.9;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTTCAGGGGG 20

Search completed: May 4, 2006, 10:07:24
Job time : 456.437 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:22:43 ; Search time 464.368 Seconds
(without alignments)
2448.208 Million cell updates/sec

Title: US-10-789-758A-5

Perfect score: 20

Sequence: 1 tccatgagcttctgagctt 20

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sv.*

12: gb_un.*

13: gb_vi.*

14: gb_hlg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX015200 Sequence
2	20	100.0	20	6	AX063579 Sequence
3	20	100.0	20	6	AX088933 Sequence
4	20	100.0	20	6	AX104695 Sequence
5	20	100.0	20	6	AX342287 Sequence
6	20	100.0	20	6	AX355545 Sequence
7	20	100.0	20	6	AX547748 Sequence
8	18.4	92.0	83194	14	AC139704 Homo sapi
9	18.4	92.0	135640	8	AC036178 Homo sapi
10	18.4	92.0	143802	9	AC139332 Mus muscu
11	18.4	92.0	143988	14	AC129500 Homo sapi
12	18.4	92.0	153094	8	CNS05TCH
13	18.4	92.0	158003	8	AC022795 Homo sapi
14	18.4	92.0	167164	9	AC148328 Mus muscu
15	18.4	92.0	170892	8	CNS07BES
16	18.4	92.0	178477	14	AC022801 Homo sapi
17	18.4	92.0	186959	8	AY191612 Pan trogl
18	18.4	92.0	195384	8	AC006499 Homo sapi

c 19	18.4	92.0	214447	9	AC122236	AC122236 Mus muscu
c 20	18.4	92.0	221360	14	AC106684	AC106684 Rattus no
c 21	18.4	92.0	233606	9	AC151908	AC151908 Mus muscu
c 22	18.4	92.0	256417	14	AC079422	AC079422 Mus muscu
c 23	18	90.0	110000	1	AY596297_12	Continuation (13 o
c 24	18	90.0	239570	9	AL831746_12	AL831746 Mouse DNA
c 25	18	90.0	275391	14	AC096242	AC096242 Rattus no
c 26	17.4	87.0	567	10	BV264373	BV264373 S235P613
c 27	17.4	87.0	643	10	BV262254	BV262254 S235P6178
c 28	17.4	87.0	2268	5	BX935505	BX935505 Gallus ga
c 29	17.4	87.0	5736	9	CR751606	CR751606 Mouse DNA
c 30	17.4	87.0	65937	14	AC102820	AC102820 Mus muscu
c 31	17.4	87.0	66843	14	AC068748	AC068748 Homo sapi
c 32	17.4	87.0	92607	8	AL583807	AL583807 Human DNA
c 33	17.4	87.0	103739	9	CR925752	CR925752 Mouse DNA
c 34	17.4	87.0	110000	15	AP008210_235	Continuation (236
c 35	17.4	87.0	110000	15	AP008211_047	Continuation (48 o
c 36	17.4	87.0	130273	15	OSJN00011	AL606447 Oryza sat
c 37	17.4	87.0	141079	8	HSR218C14	AL121894 Human DNA
c 38	17.4	87.0	152129	14	AC027416	AC027416 Homo sapi
c 39	17.4	87.0	168003	14	CR388174	CR388174 Mus muscu
c 40	17.4	87.0	178360	14	AC129234	AC129234 Rattus no
c 41	17.4	87.0	182430	14	AC118799	AC118799 Rattus no
c 42	17.4	87.0	187956	15	AC135425	AC135425 Oryza sat
c 43	17.4	87.0	199459	9	AC125192	AC125192 Mus muscu
c 44	17.4	87.0	200143	14	AC073805	AC073805 Mus muscu
c 45	17.4	87.0	203223	14	AC116077	AC116077 Rattus no

ALIGNMENTS

RESULT 1
AX015200
LOCUS AX015200 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from Patent WO9552549.
ACCESSION AX015200
VERSION AX015200.1 GI:10041243
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Friede,M. and Hermand,P.
TITLE Adjuvant compositions
JOURNAL Patent: WO 9552549-A 4 21-OCT-1999;
SMITHKLINE BEECHAM BIOLOG (BE); FRIEDE MARTIN (BE); HERMAND
PHILIPPE (BE)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCTGAGCTT 20
|||||
DB 1 TCCATGAGCTTCTGAGCTT 20
RESULT 2
AX063579
LOCUS AX063579 20 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 5 from Patent WO0100231.
ACCESSION AX063579
VERSION AX063579.1 GI:12541303
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

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other sequences; artificial sequences.
1
REFERENCE Cohen,J., Garcon,N. and Voss,G.
AUTHORS Vaccines
TITLE
JOURNAL SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAGCTT 20
Db |||||||||||||||||||
1 TCCATGAGCTTCTCTGAGCTT 20

RESULT 5
AX342287
LOCUS AX342287 20 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 2 from Patent WO0195935.
ACCESSION AX342287
VERSION AX342287.1 GI:18151774
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Davis,H.L. and Mccluskie,M.J.
TITLE Immunostimulatory nucleic acids for inducing a th2 immune response
JOURNAL Patent: WO 0195935-A 2 20-DEC-2001;
Ottawa Health Research Institute (CA) ; Coley Pharmaceutical Group,
Inc. (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAGCTT 20
Db |||||||||||||||||||
1 TCCATGAGCTTCTCTGAGCTT 20

RESULT 6
AX355545
LOCUS AX355545 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 573 from Patent WO0197843.
ACCESSION AX355545
VERSION AX355545.1 GI:18620213
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 573 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source
1..20
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/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide
phosphorothioate backbone"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;

other sequences; artificial sequences.
1
REFERENCE Cohen,J., Garcon,N. and Voss,G.
AUTHORS Vaccines
TITLE
JOURNAL SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAGCTT 20
Db |||||||||||||||||||
1 TCCATGAGCTTCTCTGAGCTT 20

RESULT 4
AX104695
LOCUS AX104695 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 887 from Patent WO0122972.
ACCESSION AX104695
VERSION AX104695.1 GI:13920892
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 887 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
source
1..20
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 7
AX547748
LOCUS
DEFINITION Sequence 887 from Patent WO02053141.
ACCESSION AX547748
VERSION AX547748.1 GI:25812892
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 887 11-JUL-2002;
FEATURES
source
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 8
AC139704/c
LOCUS
DEFINITION Homo sapiens chromosome 18 clone RP13-514J16 map 18, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC139704
VERSION AC139704.1 GI:28275005
KEYWORDS HTG; HTGS PHASE0
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Birren, B., Nuebaum, C. and Lander, E.
TITLE Homo sapiens chromosome 18, clone RP13-514J16
JOURNAL Unpublished
REFERENCE
AUTHORS Birren, B., Nuebaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collamore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Keile, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,
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Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L29418
Center clone name: 514_J_16
-----
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* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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1 912: contig of 912 bp in length
* 913 1012: gap of 100 bp
* 1013 1917: contig of 905 bp in length
* 1918 2017: gap of 100 bp
* 2018 2909: contig of 892 bp in length
* 2910 3009: gap of 100 bp
* 3010 3907: contig of 898 bp in length
* 3908 4007: gap of 100 bp
* 4008 4927: contig of 920 bp in length
* 4928 5027: gap of 100 bp
* 5028 5940: contig of 913 bp in length
* 5941 6040: gap of 100 bp
* 6041 6963: contig of 923 bp in length
* 6964 7064: gap of 100 bp
* 7064 8002: contig of 939 bp in length
* 8003 8102: gap of 100 bp
* 8103 9013: contig of 911 bp in length
* 9014 9113: gap of 100 bp
* 9114 10027: contig of 914 bp in length
* 10028 10127: gap of 100 bp
* 10128 11034: contig of 907 bp in length
* 11035 11134: gap of 100 bp
* 11135 12035: contig of 901 bp in length
* 12036 12135: gap of 100 bp
* 12136 13059: contig of 924 bp in length
* 13060 13159: gap of 100 bp
* 13160 14073: contig of 914 bp in length
* 14074 14173: gap of 100 bp
* 14174 15077: contig of 904 bp in length
* 15078 15177: gap of 100 bp
* 15178 16090: contig of 913 bp in length
* 16091 16190: gap of 100 bp
* 16191 17089: contig of 899 bp in length
* 17090 17189: gap of 100 bp
* 17190 18125: contig of 936 bp in length
* 18126 18225: gap of 100 bp
* 18226 19167: contig of 942 bp in length
* 19168 19267: gap of 100 bp
* 19268 20189: contig of 922 bp in length
* 20190 20289: gap of 100 bp
* 20290 21206: contig of 917 bp in length
* 21207 21306: gap of 100 bp
* 21307 22218: contig of 912 bp in length
```


REFERENCE
AUTHORS

3 (bases 1 to 135640)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL

Direct Submission
 Submitted (05-SEP-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE
AUTHORS

4 (bases 1 to 135640)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
 Matthews,C., McCarthy,M., Meldrum,J., Meneus,L., Mihova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
 Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
 Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL

Direct Submission
 Submitted (02-NOV-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Nov 2, 2002 this sequence version replaced gi:22726134.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9219
 Center clone name: 666_N_19

FEATURES

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Location/Qualifiers
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 /clone="RP11-666N19"
 /clone_lib="RPC1-11 Human Male BAC"
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 /rpt_family="ALR/alpha"
 9701..9961
 /rpt_family="AluJb"
 9962..10303
 /rpt_family="THE1B"
 10304..11796

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 complement(4..9444)
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 9701..9961
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 9962..10303
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 10304..11796

repeat_region
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 12103..12158
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 12159..12500
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 13135..13440
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 15192..15489
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 15592..15615
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 16618..16699
 /rpt_family="AluJ/FLAM"
 16891..17190
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 17191..17339
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 17363..17480
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 17766..17828
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 20981..21125
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 21165..21446
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 21447..21486
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 21559..21858
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 23657..23685
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 24356..25121
 /rpt_family="L1MD2"
 25113..25170
 /rpt_family="L1M4"
 25231..25282
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 25299..25543
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 25771..26537
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 26847..26886
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 27010..27146
 /rpt_family="L1ME2"
 2739T..27420
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 27685..27900
 /rpt_family="MER2"
 27925..28263
 /rpt_family="(TA)n"
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 /rpt_family="AluSg"
 28818..28854
 /rpt_family="AT_rich"

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repeat_region      complement(30885..30956)
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repeat_region      34172..34441
/rpt_family="AluJb"
repeat_region      34447..34545
/rpt_family=" (CATA)n"
repeat_region      37005..37025
/rpt_family="AT_rich"
repeat_region      complement(37371..37668)
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Best Local Similarity 95.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 106308 TCCATGAGCTTCCTGATCTT 106289

RESULT 10
AC139332/c
LOCUS
DEFINITION      AC139332 143802 bp DNA linear ROD 21-JUN-2005
Mus musculus BAC clone RP24-113C21 from chromosome 5, complete
sequence.
ACCESSION      AC139332
VERSION
KEYWORDS      HTG.
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
Trani,L., Bielicki,L. and Haglund,K.
1 (bases 1 to 143802)
Unpublished (2001)
2 (bases 1 to 143802)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (30-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 143802)
Wilson,R.K.
Direct Submission
Submitted (27-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 143802)
Wilson,R.K.
Direct Submission
Submitted (08-JUN-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 143802)
Wilson,R.K.
Direct Submission
Submitted (16-JUN-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 143802)
Wilson,R.K.
Direct Submission
Submitted (21-JUN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 8, 2005 this sequence version replaced gi:61889203.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu

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Contact: submissions@watson.wustl.edu
 ----- Summary Statistics
 Center project name: M_BB0113C21

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

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	/mol_type="genomic DNA"
	/db_xref="taxon:10090"
	/chromosome="5"
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	/clone_lib="RPCI-24"
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unsure	59170..59656
	/note="Sequence derived from one plasmid subclone."
unsure	60175..60252
	/note="Sequence derived from one plasmid subclone."
misc_feature	105406..105407
	/note="Bacterial transposon insertion in clone excised here"
unsure	124249..124255
	/note="Sequence derived from one plasmid subclone."
unsure	124429..124507
	/note="Sequence derived from one plasmid subclone."
unsure	138307..138320
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misc_feature	141288..141758
	/note="Sequence derived from PCR product of project DNA"
misc_feature	143021..143375
	/note="Sequence derived from PCR product of project DNA"

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 143802;
 Best Local Similarity 95.0%; Pred. No. 3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TCCATGAGCTTCCTGAGCTT 20

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Db 60636 TCATAAGTCTCTGAGCTT 60617
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27856
Center clone name: 1073_A_19
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 62104: contig of 62104 bp in length
* 62105: gap of 100 bp
* 123421: contig of 61217 bp in length
* 123422: gap of 100 bp
* 123521: contig of 6081 bp in length
* 123522: gap of 100 bp
* 129602: contig of 3970 bp in length
* 129603: gap of 100 bp
* 133672: contig of 4994 bp in length
* 133673: gap of 100 bp
* 138767: contig of 5122 bp in length.
* 138768: gap of 100 bp
* 138867: contig of 5122 bp in length.
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* Location/Qualifiers
* 1.143988
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* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="18"
* /map="18"
* /clone="RP11-1073A19"
* /clone_lib="RPCI-11 Human Male BAC"
* 62105..62204
* /estimated_length=100
* 123422..123521
* /estimated_length=100
* 129603..129702
* /estimated_length=100
* 133673..133772
* /estimated_length=100
* 138767..138866
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Query Match 92.0%; Score 18.4; DB 14; Length 143988;
Best Local Similarity 95.0%; Pred No. 3e+02; 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1;
QY 1 TCATGAGCTTCTCTGAGCTT 20
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Db 109658 TCATGAGCTTCTCTGAGCTT 109639
CNS05TCH 153094 bp DNA linear PRI 08-JUN-2001
Human chromosome 14 DNA sequence BAC R-241E13 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
AL355098
CNS05TCH 3 GI:13677194
VERSION AL355098.3
KEYWORDS HTG; HTGS; ACTIVEFIN
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 153094)
AUTHORS Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissbach,J.
Sequencing of the human chromosome 14
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RESULT 11
AC129500/c
LOCUS AC129500 143988 bp DNA linear HTG 27-MAR-2003
DEFINITION Homo sapiens chromosome 18 clone RP11-1073A19 map 18, 6 unordered
pieces.
ACCESSION AC129500
VERSION AC129500.3 GI:27452937
KEYWORDS HTG; HTGS; PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 143988)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-1073A19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 143988)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Keller,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 143988)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Testaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jan 1, 2003 this sequence version replaced gi:27375067.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WBIR
Web site: http://www-seq.wi.mit.edu
```


JOURNAL Submitted (15-JUL-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 167164)

AUTHORS Wilson, R.K.

TITLE Direct Submission

JOURNAL Submitted (02-SEP-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 167164)

AUTHORS Wilson, R.K.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Sep 2, 2004 this sequence version replaced gi:50300734.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: submissions@wustl.edu

----- Summary Statistics

Center project name: M_BB0329C11

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

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repeat_region 17815..17951
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repeat_region /rpt_family="MaLR"

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
||| ||||| ||||| ||||| |||||
Db 53392 TCCATGAGCTTCCTGAGCAT 53411

RESULT 15
CNS07EES/c
LOCUS
DEFINITION Human chromosome 14 DNA sequence BAC C-2506J14 of library Caltech-D
from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL445885
VERSION AL445885.1 GI:11024568
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 170892)
AUTHORS Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissbach,J.
Sequencing of the human chromosome 14
Unpublished
TITLE
JOURNAL
REFERENCE 2 (bases 1 to 170892)
AUTHORS
JOURNAL
TITLE
Submitted (27-APR-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr

-----
The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-241E13 (AC=AL355098)
Downstream BAC (overlapping the SP6 end) : R-487K10 -----
Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 8.37x in Q20 bases; sum-of-contigs -----
Overall quality chart :
Range : bases
0 :
1 - 9 : 4
10 - 19 : 78
20 - 29 : 347
30 - 39 : 859
40 - 49 : 6345
50 - 59 : 6534
60 - 69 : 7803
70 - 79 : 19454
80 - 89 : 48871
90 - 99 : 80597
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Percentage of bases with a quality value >= 40 : 99 %
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location/Qualifiers
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ORIGIN
Query Match 92.0%; Score 18.4; DB 8; Length 170892;
Best Local Similarity 95.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
||| ||||| ||||| ||||| |||||
Db 19255 TCCTTGAGCTTCCTGAGCTT 19236

Search completed: May 4, 2006, 03:51:53
Job time : 473.368 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 01:23:12 ; Search time 150.46 Seconds
(without alignments)
885.910 Million cell updates/sec

Title: US-10-789-758A-5

Perfect score: 20
Sequence: 1 tccatgagcttcctgagctt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq_21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	Aaf59505 Immunosti
2	20	100.0	20	4	Aaf99682 Immunosti
3	20	100.0	20	5	Aaf27751 P. falcip
4	20	100.0	20	6	Abk48089 Non-CpG O
5	20	100.0	20	6	Abk78403 Angiogene
6	20	100.0	20	6	Abk39151 Immunosti
7	20	100.0	20	9	Ach03223 Immunosti
8	20	100.0	20	9	Ach37184 Immunosti
9	20	100.0	20	13	Adu90203 Allergic
10	18.4	92.0	312477	12	Adp69744 Human ROC
11	17.4	87.0	2616	13	Adt16613 Plant CDN
12	17.4	87.0	12718	6	Abk52229 cDNA enco
13	17	85.0	20	2	Aav52574 Umethyla
14	17	85.0	20	2	Aav27748 Immunosti
15	17	85.0	20	2	Aav27674 Immunosti
16	17	85.0	20	2	Aaz41947 II-12 sec
17	17	85.0	20	3	Aaz48023 Immune re
18	17	85.0	20	4	Aah50578 CPG motif
19	17	85.0	20	4	Aah19258 Phosphoro

20	17	85.0	20	4	Aaf98908	Immunosti
21	17	85.0	20	4	Aaf99075	Immunosti
22	17	85.0	20	4	Aaf98967	Immunosti
23	17	85.0	20	4	Aaf99666	Immunosti
24	17	85.0	20	6	Abk78387	Angiogene
25	17	85.0	20	6	Abk77543	Angiogene
26	17	85.0	20	6	Abk77608	Angiogene
27	17	85.0	20	6	Abk77716	Angiogene
28	17	85.0	20	6	Abk39152	Immunosti
29	17	85.0	20	6	Abk39153	Immunosti
30	17	85.0	20	6	Abk39154	Immunosti
31	17	85.0	20	6	Abk70609	Dendritic
32	17	85.0	20	8	Abk222889	Phosphoro
33	17	85.0	20	9	Adp99341	Immunosti
34	17	85.0	20	9	Adp99507	Immunosti
35	17	85.0	20	9	Adh03207	Immunosti
36	17	85.0	20	9	Adb36469	Immunosti
37	17	85.0	20	9	Adb36577	Immunosti
38	17	85.0	20	9	Adb36410	Immunosti
39	17	85.0	20	9	Adb37168	Immunosti
40	17	85.0	20	10	Aad60259	Oligonucl
41	17	85.0	20	10	Adg68110	Umethyla
42	17	85.0	20	12	Adi01050	Immunosti
43	17	85.0	20	12	Adm99019	Immunosti
44	17	85.0	20	12	Ado04735	CpG oligo
45	17	85.0	20	12	Adq07614	Nucleotid

ALIGNMENTS

RESULT 1

Aaf59505

ID Aaf59505 standard; DNA; 20 BP.

XX AAF59505;

DT 24-APR-2001 (first entry)

XX Immunostimulatory oligonucleotide WD1005 for use in an HIV vaccine.

XX Immunostimulatory oligonucleotide; adjuvant; HIV antigen; HIV infection; vaccine; prophylaxis; treatment; ss.

OS Synthetic.

PN WO200100232-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-EP005998.

XX 29-JUN-1999; 99GB-00015205.

PR 31-JAN-2000; 2000GB-00002200.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Garcon N, Voss G;

XX WPI; 2001-122974/13.

XX New vaccine formulation comprising human immunodeficiency virus (HIV) antigen and immunostimulatory CpG oligonucleotide, useful for preventing and treating HIV infections in a patient.

PS Claim 10; Page 17; 23pp; English.

XX The invention relates to an HIV vaccine comprising an HIV antigen and an immunostimulatory oligonucleotide (AAF59501-AAF59508). With the exception of oligonucleotide WD1005 (AAF59505), the immunostimulatory oligonucleotides contain at least one unmethylated CpG motif. In preferred embodiments the internucleotide linkage is phosphorothioate, although phosphodiester and other internucleotide bonds, or mixtures of

CC linkages are within the scope of the invention. The HIV antigen may be selected from gp160, gp120, Nef, Tat, and Nef or Tat derivatives or fusion proteins. The vaccine is used for the prophylaxis or treatment of HIV infection in a patient. The present sequence represents a specifically claimed immunostimulatory oligonucleotide, WD1005, for use in the vaccine of the invention. This oligonucleotide does not contain a CpG motif

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 2
AAF99682
ID AAF99682 standard; DNA; 20 BP.
XX
XX AAF99682;
AC
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #798.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
PR
XX 27-SEP-1999; 99US-0156135P.
PR
XX 23-AUG-2000; 2000US-0227436P.
PR
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
PT
XX
XX Claim 101; Page 55; 338pp; English.
PS
XX
XX The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 3
AAF27751
ID AAF27751 standard; DNA; 20 BP.
XX
XX AAF27751;
AC
XX
DT 03-APR-2001 (first entry)
XX
DE P. falciparum vaccine CpG oligonucleotide WD1005.
XX
XX Plasmodium falciparum; malaria; CpG oligonucleotide; vaccine; sporozoite; KW ds.
XX
OS Unidentified.
XX
XX WO200100231-A2.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 23-JUN-2000; 2000WO-EP005841.
PF
XX
XX 29-JUN-1999; 99GB-00015204.
PR
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Cohen J, Garcon N, Voss G;
PI
XX
XX WPI; 2001-112392/12.
DR
XX
XX New vaccine formulation, useful for preventing and treating plasmodium infection in a patient, comprises malaria antigen and immunostimulatory CpG oligonucleotide.
PT
XX
XX Claim 8; Page 16; 22pp; English.
PS
XX
XX The present invention describes a vaccine comprising a malaria antigen and an immunostimulatory CpG oligonucleotide. This is useful in the prevention and treatment of malaria caused by Plasmodium falciparum infection
CC
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 4
ABK48089
ID ABK48089 standard; DNA; 20 BP.
XX
XX ABK48089;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Non-CpG oligonucleotide motif #2 used to induce a Th2 immune response.
DE
XX
XX Non-autoimmune Th1 mediated disease; autoimmune disease; cancer;

KW infectious disease; Th1 immune response; rheumatoid arthritis;
 KW Crohn's disease; systemic lupus erythematosus; SLE; myasthenia gravis;
 KW Hashimoto's thyroiditis; Goodpasture's syndrome; pemphigus;
 KW Grave's disease; autoimmune haemolytic anaemia; scleroderma;
 KW autoimmune thrombocytopenic purpura; mixed connective tissue disease;
 KW polymyositis; pernicious anaemia; idiopathic Addison's disease;
 KW autoimmune-associated infertility; glomerulonephritis; psoriasis;
 KW bullous pemphigoid; Sjogren's syndrome; insulin resistance;
 KW diabetes mellitus; inflammatory disorder; organ allograft rejection;
 KW Hepatitis B infection; unexplained recurrent abortion;
 KW parasitic infection; non-CpG motif; ss.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 XX
 XX US200104416-A1.
 XX
 XX 22-NOV-2001.
 XX
 XX 22-JAN-2001; 2001US-00768012.
 XX
 XX 20-JAN-2000; 2000US-0177461P.
 XX
 XX (MCCL/) MCCLUSKIE M J.
 XX (DAVI/) DAVIS H L.
 XX
 XX Mccluskie MJ, Davis HL;
 XX
 XX WPI; 2002-138610/18.
 XX
 XX
 XX Inducing an antigen specific immune response useful in treating Th1-
 PT mediated inflammatory disorders, e.g., (non)-autoimmune diseases or
 PT cancer, comprises administering a Th2-immunostimulatory nucleic acid and
 PT an antigen.
 XX
 XX Example; Page 27; 50pp; English.
 XX
 CC The invention relates to methods using a Th2-immunostimulatory nucleic
 CC acid to induce an antigen specific response by administration mucosally,
 CC dermally or parenterally with an antigen, to stimulate an antibody
 CC dependent cellular cytotoxic immune response, to treat non-autoimmune Th1
 CC mediated disease and autoimmune disease, to prevent infectious diseases
 CC and cancer. The methods are useful for treating and preventing disorders
 CC associated with a Th1 immune response, or for creating a Th2 environment
 CC for treating disorders that are sensitive to a Th2 immune response. Th1-
 CC mediated disorders include autoimmune diseases (e.g., rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus (SLE),
 CC autoimmune encephalomyelitis, myasthenia gravis, Hashimoto's thyroiditis,
 CC Goodpasture's syndrome, pemphigus, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenic purpura, scleroderma with anti-
 CC collagen antibodies, mixed connective tissue disease, polymyositis,
 CC pernicious anaemia, idiopathic Addison's disease, autoimmune-associated
 CC infertility, glomerulonephritis, bullous pemphigoid, Sjogren's syndrome,
 CC insulin resistance, and autoimmune diabetes mellitus) and non-autoimmune
 CC diseases (e.g., psoriasis, Th1 inflammatory disorders, solid organ
 CC allograft rejection, symptoms associated with Hepatitis B infection,
 CC insulin-dependent diabetes mellitus, multiple sclerosis, silent
 CC thyroiditis, and unexplained recurrent abortion). The methods are also
 CC useful for treating or preventing parasitic infections, infectious
 CC diseases, cancer, for stimulating antibody dependent cellular cytotoxic
 CC immune response and for inducing an antigen specific response. The
 CC present sequence represents a non-CpG oligonucleotide motif used to
 CC induce a Th2 immune response as described in the methods of the invention
 XX
 XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGAGCTTCCTGAGCTT 20
 ||||||||||||||||
 Db 1 TCCATGAGCTTCCTGAGCTT 20
 ||||||||||||||||
 RESULT 5
 ABS78403
 ID ABS78403 standard; DNA; 20 BP.
 XX
 AC ABS78403;
 XX
 XX 13-DEC-2002 (first entry)
 XX
 XX Angiogenesis inhibitory oligonucleotide #887.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 XX WO200253141-A2.
 XX
 XX 11-JUL-2002.
 XX
 XX 14-DEC-2001; 2001WO-US048459.
 XX
 XX 14-DEC-2000; 2000US-0255534P.
 XX
 XX (COLE-) COLEY PHARM GROUP INC.
 XX
 XX Bratzler RL;
 XX
 XX WPI; 2002-566690/60.
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 35; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGAGCTTCCTGAGCTT 20
 ||||||||||||||||
 Db 1 TCCATGAGCTTCCTGAGCTT 20
 ||||||||||||||||

```

RESULT 6
ABL39151
ID ABL39151 standard; DNA; 20 BP.
XX
XX ABL39151;
AC
XX
DT 16-APR-2002 (first entry)
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 573.
DE
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT FT
FT /note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
PN
XX
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020154.
XX
XX 22-JUN-2000; 2000US-0213346P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G;
PI
XX
XX WPI; 2002-154611/20.
DR
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 241; 312pp; English.
PS
XX
XX The present invention relates to methods for treating or preventing
XX cancer, involving administering to a subject having or at risk of
XX developing cancer immunostimulatory nucleic acids that induce expression
XX of cell surface antigens and antibodies. The methods are useful for
XX treating or preventing cancer such as basal cell carcinoma, bladder
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX breast cancer, cervical cancer, colon and rectum cancer, connective
XX tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX present sequence is an immunostimulatory oligonucleotide described in the
XX exemplification of the invention
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
Db |||||
1 TCCATGAGCTTCCTGAGCTT 20

RESULT 7
ACH03223
ID ACH03223 standard; DNA; 20 BP.
XX
XX ACH03223;
AC

```

```

XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #858.
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
OS
XX US2003050268-A1.
XX
XX 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
XX (KRIE/) KRIEG A M.
XX (BERG/) BERG D J.
XX
XX Krieg AM, Berg DJ;
PI
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 32; 229pp; English.
PS
XX
XX The invention describes a method of treating non-allergic inflammatory
XX disease comprising administering to a subject having or at risk of
XX developing a non-allergic inflammatory disease an immunostimulatory
XX nucleic acid for prevention or treatment of the disease. The method is
XX useful for treating non-allergic inflammatory diseases, such as
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX This sequence represents an immunostimulatory nucleic acid
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
Db |||||
1 TCCATGAGCTTCCTGAGCTT 20

RESULT 8
ADB37184
ID ADB37184 standard; DNA; 20 BP.
XX
XX ADB37184;
AC
XX
XX 04-DEC-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #798.
XX
XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
XX Synthetic.
OS
XX US2003087848-A1.
XX
XX 08-MAY-2003.
XX
XX 02-FEB-2001; 2001US-00776479.
XX

```


XX PR 03-FEB-2000; 2000US-0179991P.
XX PA (BRAT/) BRATZLER R L.
XX PA (PETE/) PETERSEN D M.
XX PA (FOUR/) FOURON Y.
XX PI Bratzler RL, Petersen DM, Fouron Y;
XX WPI; 2003-657977/62.
XX DR Treating and/or preventing allergy or asthma using an immunostimulatory
XX PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX PS Disclosure; Page 17; 221pp; English.
XX CC The invention relates to a method of treating or preventing allergy or
XX CC asthma which comprises administering to a subject a poly-G nucleic acid
XX CC in an aerosol formulation. The methods and compositions of the present
XX CC invention are useful for diagnosing and/or treating asthma and allergy
XX CC especially in a hypo-responsive subject. The present sequence represents
XX CC an immunostimulatory nucleic acid of the invention.
XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAGCTT 20
DB 1 TCCATGAGCTTCCTGAGCTT 20
RESULT 9
ADU90203
ID ADU90203 standard; DNA; 20 BP.
XX AC ADU90203;
XX DT 10-FEB-2005 (first entry)
XX DE Allergic response suppressor oligonucleotide #887.
XX KW ss; antiasthmatic; anti-allergic; dermatological; anti-inflammatory;
XX KW antibacterial; virucide; immunoglobulin E antagonist; allergy;
XX KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;
XX KW bacterial infection; viral infection.
XX OS Synthetic.
XX PN US2004235774-A1.
XX PD 25-NOV-2004.
XX PF 23-APR-2004; 2004US-00831778.
XX PR 03-FEB-2000; 2000US-0179991P.
XX PR 02-FEB-2001; 2001US-00776479.
XX PA (BRAT/) BRATZLER R L.
XX PA (PETE/) PETERSEN D M.
XX PA (FOUR/) FOURON Y.
XX PI Bratzler RL, Petersen DM, Fouron Y;
XX WPI; 2004-833006/82.
XX DR Suppressing allergies, including asthma, rhinitis, urticaria and atopic
XX PT dermatitis, in a subject, comprises administering a first and second dose
XX PT of an immunostimulatory nucleic acid.
XX PS Disclosure; SEQ ID NO 887; 235pp; English.

XX CC The invention relates to a method of suppressing a symptom of an allergic
XX CC response in a subject by administering a first and second dose of an
XX CC immunostimulatory nucleic acid that comprises a nucleotide sequence
XX CC comprising 5'-cg-3', and where the second dose is administered from 1 day
XX CC to 8 weeks after the first dose. The methods and compositions of the
XX CC present invention are useful for the treatment or prevention of asthma
XX CC and allergy, including rhinitis, urticaria and atopic dermatitis, using
XX CC an immunostimulatory nucleic acid alone or in combination with other
XX CC medications. They can also be used in preventing bacterial and viral
XX CC infections. This sequence represents an oligonucleotide used in the
XX CC method of the invention.
XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAGCTT 20
DB 1 TCCATGAGCTTCCTGAGCTT 20
RESULT 10
ADP69744
ID ADP69744 standard; DNA; 312477 BP.
XX AC ADP69744;
XX DT 09-SEP-2004 (first entry)
XX DE Human ROCK 1 DNA #2.
XX KW ds; gene; human; ROCK 1; hyperproliferative disorder; cancer.
XX OS Homo sapiens.
XX PN US2004115641-A1.
XX PD 17-JUN-2004.
XX PF 11-DEC-2002; 2002US-00317883.
XX PR 11-DEC-2002; 2002US-00317883.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowseert LM, Dobie KW;
XX WPI; 2004-449381/42.
XX PT New oligonucleotide compound that inhibits expression of ROCK 1, useful
XX PT for preparing a composition for treating hyperproliferative disorder,
XX PT e.g., cancer.
XX PS Example 15; SEQ ID NO 11; 195pp; English.
XX CC The invention relates to a new compound, targeted to a nucleic acid
XX CC encoding ROCK 1, that specifically hybridises with the nucleic acid
XX CC encoding ROCK 1 and inhibits expression of ROCK 1. The oligonucleotide
XX CC compound is useful for preparing a composition for treating
XX CC hyperproliferative disorder, e.g. cancer. The present sequence represents
XX CC human ROCK 1 DNA.
XX SQ Sequence 312477 BP; 92110 A; 58460 C; 60155 G; 98196 T; 0 U; 3556 Other;
Query Match 92.0%; Score 18.4; DB 12; Length 312477;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||

Db 184253 TCCATGAGCTTCTGATCTT 184272

RESULT 11

ADT16613/c

ID ADT16613 standard; cDNA; 2616 BP.

XX

AC ADT16613;

XX

DT 13-JAN-2005 (first entry)

XX

DE Plant cDNA, Seq ID 1939.

XX

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;

KW drought tolerance; disease resistance; galactomanan production;

KW plant growth regulator; heat tolerance; herbicide tolerance;

KW lignin production; extreme osmotic condition tolerance;

KW pathogen resistance; pest resistance; yield improvement; seed oil yield;

XX seed protein yield.

XX

OS Viridiplantae.

XX

PN US2004216190-A1.

XX

PD 28-OCT-2004.

XX

XX 18-DEC-2003; 2003US-00739930.

PF

XX 28-APR-2003; 2003US-00424599.

PR

XX 28-APR-2003; 2003US-00425115.

XX

XX (KOVA/) KOVALIC D K.

PA

XX Kovalic DK;

PI

XX WPI; 2004-757369/74.

DR

XX New recombinant DNA constructs useful in the field of biochemistry and

PT Genetic, and in particular for producing transgenic plants with improved

PT biological characteristics.

XX

PS Claim 1; SEQ ID NO 1939; 14pp; English.

XX

XX The invention relates a recombinant DNA construct comprising a

CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:

CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences

CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,

CC Arabidopsis, wheat and rape but the specification does not indicate which

CC sequences is derived from which organism. Also included is a method of

CC producing a plant having an improved property, comprising transforming a

CC plant with a recombinant DNA construct comprising a promoter region

CC functional in a plant cell operably joined to a polynucleotide encoding a

CC polypeptide associated with the property, and growing the transformed

CC plant. The property is selected from improving plant cold tolerance, for

CC manipulating growth rate in plant cells by modification of the cell cycle

CC pathway, for improving plant drought tolerance, for providing increased

CC resistance to plant disease, for galactomanan production, for production

CC of plant growth regulators, for improving plant heat tolerance, for

CC improving plant tolerance to herbicides, for increasing the rate of

CC homologous recombination in plants, for lignin production, for improving

CC plant tolerance to extreme osmotic conditions, for improving plant

CC tolerance to pathogens or pests, for yield improvement by modification of

CC photoynthesis, for modifying seed oil yield and/or content, for

CC modifying seed protein yield and/or content, for yield improvement by

CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake

CC and for yield improvement by providing improved plant growth and

CC development under at least one stress condition. The polynucleotide may

CC also encode a plant transcription factor. The methods and compositions of

CC the present invention are useful in the field of biochemistry and

CC genetics, in particular for producing transgenic plants with improved

CC biological characteristics such as increased yield, improved nitrogen

CC flow, increasing plant tolerance to cold or heat, improving plant

CC tolerance to extreme osmotic and drought conditions, and improving plant

CC

CC tolerance to plant pests or pathogens. They can also be used in physical

CC arrays of molecules, plant breeding markers, computer-based storage and

CC analysis systems. The present sequence is one of the 5544 plant cDNA

CC sequences of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?docID=20040216190.

XX

SQ Sequence 2616 BP; 733 A; 583 C; 657 G; 643 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 13; Length 2616;

Best Local Similarity 94.7%; Pred. No. 3.3e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTGAGCTT 20

DB 312 CCATGAGCTCCTGAGCTT 294

RESULT 12

ABKS2229/c

ID ABKS2229 standard; cDNA; 12718 BP.

XX

AC ABKS2229;

XX

DT 13-AUG-2002 (first entry)

XX

DE cDNA encoding human CYP27A1 protein.

XX

XX Human; Cytochrome P450; Subfamily XXVIIA; single nucleotide polymorphism;

KW Steroid 27-Hydroxylase; Cerebrotendinous Xanthomatosis Polypeptide 1;

KW CYP27A1, SNP; drug screening; cerebrotendinous xanthomatosis;

KW Chromosome 2q33-qter; gene; ss.

XX

OS Homo sapiens.

XX

XX Key

FT variation

FT

FT Location/Qualifiers

FT replace(564,C)

FT /tag= a

FT /standard_name= "Single Nucleotide Polymorphism (SNP)"

FT /note= "Polymorphic site 1 (PS1)"

FT CDS

FT 1001..8719

FT /tag= c

FT /product= "Human CYP27A1 protein"

FT exon

FT 1001..1255

FT /tag= b

FT /number= 1

FT intron

FT 1256..3409

FT /tag= d

FT /number= 1

FT variation

FT replace(1342,A)

FT /tag= e

FT /standard_name= "Single Nucleotide Polymorphism (SNP)"

FT /note= "Polymorphic site 2 (PS2)"

FT exon

FT 3410..3600

FT /tag= f

FT /number= 2

FT variation

FT replace(3564,A)

FT /tag= g

FT /standard_name= "Single Nucleotide Polymorphism (SNP)"

FT /note= "Polymorphic site 3 (PS3)"

FT variation

FT replace(3592,A)

FT /tag= h

FT /standard_name= "Single Nucleotide Polymorphism (SNP)"

FT /note= "Polymorphic site 4 (PS4)"

FT intron

FT 3601..5910

FT /tag= i

FT /number= 2

FT variation

FT replace(3611,A)

FT /tag= j

FT /standard_name= "Single Nucleotide Polymorphism (SNP)"

FT /note= "Polymorphic site 5 (PS5)"

FT variation

FT replace(5770,G)

```
FT /tag= k
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 6 (PS6)"
FT exon 5911..6110
FT /tag= 1
FT /number= 3
FT variation replace(5970,T)
FT /tag= m
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 7 (PS7)"
FT variation replace(5988,T)
FT /tag= n
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 8 (PS8)"
FT intron 6111..6240
FT /tag= o
FT /number= 3
FT exon 6241..6438
FT /tag= p
FT /number= 4
FT intron 6439..6612
FT /tag= q
FT /number= 4
FT exon 6613..6785
FT /tag= r
FT /number= 5
FT variation replace(6689,A)
FT /tag= s
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 9 (PS9)"
FT intron 6786..7709
FT /tag= t
FT /number= 5
FT variation replace(6843,T)
FT /tag= u
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 10 (PS10)"
FT exon 7710..7876
FT /tag= v
FT /number= 6
FT variation replace(7843,T)
FT /tag= w
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 11 (PS11)"
FT intron 7877..8068
FT /tag= x
FT /number= 6
FT variation replace(7931,C)
FT /tag= y
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 12 (PS12)"
FT variation replace(8003,C)
FT /tag= z
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 13 (PS13)"
FT exon 8069..8147
FT /tag= aa
FT /number= 7
FT intron 8148..8233
FT /tag= ab
FT /number= 7
FT exon 8234..8446
FT /tag= ac
FT /number= 8
FT variation replace(8441,T)
FT /tag= ad
FT /standard_name= "Single Nucleotide Polymorphism (SNP)"
FT /note= "Polymorphic site 14 (PS14)"
FT intron 8447..8599
FT /tag= ae
FT /number= 8
FT exon 8600..8719
FT /tag= af
```

```
FT /number= 9
XX WO200230952-A2.
XX 18-APR-2002.
XX
XX 15-OCT-2001; 2001WO-US042727.
XX
XX 13-OCT-2000; 2000US-0239942P.
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Anastasio AE, Chew A, Han J, Sanchis A;
XX WPI; 2002-435436/46.
XX P-PSDB; AAU97675.
XX
XX Novel isolated human Cytochrome P450, Subfamily XXVIIA, Steroid 27-
XX Hydroxylase, Cerebrotendinous Xanthomatosis 1 gene, useful for
XX therapeutic purposes, and for studying expression and function of the
XX gene.
XX
XX Claim 1; Fig 1; 90pp; English.
XX
XX The present invention relates to a new human Cytochrome P450, Subfamily
XX XXVIIA, (Steroid 27-Hydroxylase, Cerebrotendinous Xanthomatosis)
XX polypeptide 1 (CYP27A1) polynucleotide. The polynucleotide of the
XX invention comprises a sequence which is a polymorphic variant for a
XX reference sequence for the CYP27A1 gene or its fragment, or a polymorphic
XX variant of a reference sequence for a CYP27A1 cDNA or its fragment. The
XX invention is useful for screening for drugs by contacting the CYP27A1
XX polymorphic variant with a candidate agent and assaying for binding
XX activity. The invention is also useful in studying the expression and
XX function of CYP27A1, and in expressing CYP27A1 protein for use in
XX screening for candidate drugs to treat diseases related to CYP27A1
XX activity, e.g. cerebrotendinous xanthomatosis. Other uses include for
XX therapeutic purposes and for studying expression of the CYP27A1 isogenes
XX in vivo, for in vivo screening and testing of drugs targeted against
XX CYP27A1 protein, and for testing the efficacy of therapeutic agents and
XX compounds for diseases associated with CYP27A1 activity, e.g.
XX cerebrotendinous xanthomatosis, in a biological system. The invention is
XX useful for studying the effect of the variation on the biological
XX activity of CYP27A1 as well as on the binding affinity of candidate drugs
XX targeting CYP27A1 for the treatment of cerebrotendinous xanthomatosis.
XX The present nucleic acid sequence represents the human CYP27A1 gene
XX located on chromosome 2q33-qter. This sequence encodes the human CYP27A1
XX protein of the invention
XX
XX Sequence 12718 BP; 3189 A; 2997 C; 3093 G; 3225 T; 0 U; 214 Other;
XX
XX Query Match 87.0%; Score 17.4; DB 6; Length 12718;
XX Best Local Similarity 94.7%; Pred. No. 4e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 CCATGAGCTTCCTGAGCTT 20
XX ||||| ||||| |||||
XX Db 2833 CCATGAGTTTCTCGAGCTT 2815
XX
XX RESULT 13
XX AAV52574
XX ID AAV52574 standard; DNA; 20 BP.
XX
XX AC AAV52574;
XX
XX DT 20-NOV-1998 (first entry)
XX
XX DE Unmethylated CpG dinucleotide.
XX
XX KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
XX natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
XX pulmonary disorder; asthma; environmentally induced airway disease;
XX bacterial infection; endotoxaemia; therapy; cystic fibrosis;
```


PI Krieg AM, Kline JN;
XX
DR WPI; 1998-272127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at least one
PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
PT or autoimmune disease.
XX
XX
PS Disclosure; Page 11; 109pp; English.
XX
XX AAV27641-751 represent immunostimulatory oligodeoxynucleotides (ODNs)
CC of the invention. The ODNs contain at least one unmethylated CpG
CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
CC thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCG tetramer
CC or more than one CCG or CGG trimer OR 5' NX1X2CGX3X4N 3', where at least
CC one nucleotide separates consecutive CpGs, X1 and X2 are selected from
CC GpT, GpG, GpA, ApT and ApA, X3 and X4 are selected from Tpt or Cpt, N is
CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
CC does not contain a CCG tetramer or more than one CCG or CGG trimer. The
CC ODNs activate lymphocytes in a subject and redirect a subject's immune
CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other
CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
CC The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune diseases, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a
CC human
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 1 TCCATGAGCTTCCTGAG 17

Search completed: May 4, 2006, 02:44:17
Job time : 154.46 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:45:02 ; Search time 1417.59 Seconds
(without alignments)
660.095 Million cell updates/sec

Title: US-10-789-758A-5

Perfect score: 20
Sequence: 1 tccatgagcttcctgagctt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	581	10	CG064553
2	19	95.0	593	7	CR291334
3	19	95.0	748	8	DT075398
4	18.4	92.0	411	7	CF858979
5	18.4	92.0	465	3	BP084928
6	18.4	92.0	520	7	CF850403
7	18.4	92.0	568	9	AZ474937
8	18.4	92.0	584	6	CB291961
9	18.4	92.0	645	10	C2222277
10	18.4	92.0	661	9	CC510758
11	18.4	92.0	854	9	BH120643
12	17.4	87.0	202	9	BH640052
13	17.4	87.0	298	5	BU097976
14	17.4	87.0	316	9	CC096512
15	17.4	87.0	367	11	DE127737
16	17.4	87.0	376	7	CK401820
17	17.4	87.0	415	3	BM028315
18	17.4	87.0	418	2	BE212988
19	17.4	87.0	418	3	BM028520
20	17.4	87.0	421	3	BM028472
21	17.4	87.0	421	3	BM028681
22	17.4	87.0	423	7	CK423072

C 23	17.4	87.0	436	7	CK411648
C 24	17.4	87.0	438	7	CK421251
C 25	17.4	87.0	442	2	BE470037
C 26	17.4	87.0	442	2	BE470038
C 27	17.4	87.0	442	2	CF971751
C 28	17.4	87.0	448	3	BM028300
C 29	17.4	87.0	464	2	BE469162
C 30	17.4	87.0	467	9	AQ592441
C 31	17.4	87.0	470	10	CZ091131
C 32	17.4	87.0	473	1	AW280520
C 33	17.4	87.0	473	8	CV995382
C 34	17.4	87.0	493	7	CK411146
C 35	17.4	87.0	493	7	CK411948
C 36	17.4	87.0	497	7	CK425086
C 37	17.4	87.0	498	9	AQ294613
C 38	17.4	87.0	539	3	BM028888
C 39	17.4	87.0	539	3	BM029009
C 40	17.4	87.0	565	5	BX924669
C 41	17.4	87.0	594	6	CA830455
C 42	17.4	87.0	622	9	AZ967380
C 43	17.4	87.0	624	10	CL969124
C 44	17.4	87.0	631	7	CK051754
C 45	17.4	87.0	637	5	BU385990

ALIGNMENTS

RESULT 1
CG064553
LOCUS
CG064553
DEFINITION
CG064553
ACCESSION
CG064553.1
VERSION
GI:33936733
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
REFERENCE
1 (bases 1 to 581)
AUTHORS
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Benmetzen, J.
TITLE
Maize Genomics Consortium
JOURNAL
Unpublished (2003)
COMMENT
Other GSSs: FUICX67TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1..581
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0554L14"
/clone.lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site: 1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"

CG064553
FUICX67TB ZM 0.6 1.0 KB
Zea mays genomic clone ZMMBTa0554L14,
genomic survey sequence.

CG064553
GI:33936733
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 581)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Benmetzen, J.

Maize Genomics Consortium
Unpublished (2003)

Other GSSs: FUICX67TD
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

Location/Qualifiers
1..581
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0554L14"
/clone.lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site: 1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"

Query Match
Best Local Similarity 95.0%; Score 19; DB 10; Length 581;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 CCATGAGCTTCTCTGAGCTT 20

```

Db      388 CCATGAGCTTCTCTGAGCTT 406
|||||
RESULT 2
CR291334/c
LOCUS   CR291334 Oryza sativa library (Han B) Oryza sativa cDNA clone
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 593)
AUTHORS
Han,B., Peng,Q., Huang,Y.C., Ying,K., Li,Y., Guan,J.P., Zhu,J.J.,
Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L.,
Weng,Q.J., Zhang,B., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T.,
Zhang,Y.J., Lu,Y., Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X.,
Zhang,L., Lan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.
Rice cDNA EST clone
JOURNAL
TITLE
Unpublished (2003)
COMMENT
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, China
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cDNA est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
1..593
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone_lib="Oryza sativa library (Han B)"

FEATURES
source
1..593
Query Match 95.0%; Score 19; DB 7; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTCTGAGCTT 20
|||||
Db 87 CCATGAGCTTCTCTGAGCTT 69
|||||

RESULT 3
DT075398
LOCUS   DT075398 748 bp mRNA linear EST 11-AUG-2005
DEFINITION
AGENCOURT 55788292 NICHG XGC FAbN Xenopus laevis cDNA clone
IMAGE:8076153 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 748)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapsb-x@mail.nih.gov

Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17359 row: 1 column: 07
High quality sequence stop: 597.
Location/Qualifiers
1..748
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8076153"
/lab_host="DH10B Tona"
/clone_lib="NICHG XGC FAbN"
/note="Organ: fat body; Vector: pExpress-1; Site 1: EcorV;
Site 2: NotI; cDNA was primed using oligo-dT primer;
5'-TGACTAGTTCTAGATCGAGCGGCC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection 1.2kb
resulted in an average insert size of 1.5kb, and Cot value
of 7. This is a normalized library (primary library is
NICHG XGC FAb) and was constructed by Express Genomics
(Frederick, MD). Note: this is a (
http://xgc.nci.nih.gov/) Xenopus Gene Collection library."

ORIGIN
Query Match 95.0%; Score 19; DB 8; Length 748;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTCTGAGCTT 20
|||||
Db 571 CCATGAGCTTCTCTGAGCTT 589
|||||

RESULT 4
CF858979/c
LOCUS   CF858979 411 bp mRNA linear EST 31-OCT-2003
DEFINITION
psZG004xG16f USDA-IPAFS:Expression of Phytophthora sojae genes
during infection and propagation_sZG Phytophthora sojae cDNA clone
szG004G16 5, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytophthora sojae
Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
1 (bases 1 to 411)
AUTHORS
Tyler,B.
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtylev@vt.edu
PCR Primers
FORWARD: M13 reverse 17mer at 5' end
BACKWARD: M13 reverse 17mer at 5' end
Plate: 004 row: G column: 16
Seq primer: M13 reverse 17mer at 5' end
High quality sequence stop: 411.
Location/Qualifiers
1..411
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="szG004G16"
/tissue_type="Zoospore"

FEATURES
source
1..411

```



```

/cell_line="P6497"
/dev_stage="Zoospore"
/lab_host="synthetic medium"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_s2G"
/note="Vector: PCMV-SPORT6.1; Site_1: SalI; Site_2: NotI"

```

ORIGIN

```

Query Match      92.0%; Score 18.4; DB 7; Length 411;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
DB 64 TCCATGAGCTTCCTGAGCTT 45
    |||||

```

RESULT 5

```

BP084928/c
LOCUS BP084928 Lotus japonicus roots 465 bp mRNA linear EST 27-AUG-2004
DEFINITION cDNA clone MRL023h07_f_3', mRNA sequence.
ACCESSION BP084928
VERSION BP084928.1 GI:45641588
KEYWORDS EST.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.
1 (bases 1 to 465)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Characteristics of the Lotus japonicus gene repertoire deduced from
large-scale expressed sequence tag (EST) analysis
Plant Mol. Biol. 54 (3), 405-414 (2004)
15284495
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/.

```

FEATURES

```

source
1..465
/organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/isolate="Miyakojima MG-20"
/db_xref="taxon:34305"
/clone="MRL023h07.f"
/tissue_type="roots"
/clone_lib="Lotus japonicus roots"

```

ORIGIN

```

Query Match      92.0%; Score 18.4; DB 3; Length 465;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
DB 311 TCCATGAGCTTCAGAGCTT 292
    |||||

```

RESULT 6

```

CF850403/c
LOCUS CF850403 520 bp mRNA linear EST 30-OCT-2003
DEFINITION psMA014xBl2f USDA-IFAFS:Expression of Phytophthora sojae genes
during infection and propagation_sMA Phytophthora sojae cDNA clone
sMA014B12 5, mRNA sequence.
ACCESSION CF850403
VERSION CF850403.1 GI:38066057
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM

```

```

Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 520)
Tyler,B.
Tyler,B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmt Tyler@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 014 row: B column: 12
Seq primer: BK reverse primer
High quality sequence stop: 520.
Location/Qualifiers
1..520
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sMA014B12"
/tissue_type="mycelium"
/cell_line="P6497"
/dev_stage="synthetic medium"
/lab_host="synthetic medium"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_sMA"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

```

FEATURES

```

source

```

ORIGIN

```

Query Match      92.0%; Score 18.4; DB 7; Length 520;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
DB 96 TCCATGAGCTTCCTGAGCTT 77
    |||||

```

RESULT 7

```

AZ474937/c
LOCUS AZ474937 568 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0292K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0292K09 R, genomic survey sequence.
ACCESSION AZ474937
VERSION AZ474937.1 GI:10633062
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM

```

ORIGIN

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 568)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0292 row: K column: 09

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Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 568.

Location/Qualifiers

FEATURES

source

1..568
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0292K09"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 568;

Best Local Similarity 95.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGAGCTTCTGAGCTT 20

Db 538 TCATGAGCTTCTGAGCAT 519

RESULT 8

CB291961

LOCUS

DEFINITION

CB291961 584 bp mRNA linear EST 28-FEB-2003
UCRCS01_03ch11_b1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_03ch11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Citrus sinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Rosids; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 584)

Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R.,

Kudrna, D., Wanamaker, S., Wing, R., and Yu, Y.

Development of EST Resources and New Genetic Markers for California

Citrus

Unpublished (2003)

Contact: Timothy Close

Department of Botany & Plant Sciences, University of California

Riverside, CA, 92521-0124

Tel: 9097873318

Fax: 9097874437

Email: timothy.close@ucr.edu

Seq primer: T7.

Location/Qualifiers

1..584

/organism="Citrus sinensis"

FEATURES

source

/mol_type="mRNA"
/cultivar="Washington navel"
/db_xref="taxon:2711"
/clone="UCRCS01_03ch11"
/tissue_type="Rind containing flavedo and albedo"
/dev_stage="Mature fruit"
/lab_host="E. coli TJC121"
/clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarVest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 584;

Best Local Similarity 95.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGAGCTTCTGAGCTT 20

Db 196 TCATGAGCTTCTGGGCTT 215

RESULT 9

CB222277/c

LOCUS

DEFINITION

CB222277 645 bp DNA linear GSS 10-FEB-2005
A1AA-aac60f07.g1 Ancylostoma caninum whole genome shotgun library (A1AAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ancylostoma caninum (dog hookworm)

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;

Ancylostomatoidae; Ancylostomatinae; Ancylostoma.

1 (bases 1 to 645)

Mitreva, M., McCarter, J.P., Pape, D., Ritter, E., Tsagarisvili, R.,

Ronko, I., Martin, J., Wylie, T., Dante, M., Meyer, R., Messina, D.,

Waterston, R.H., Clifton, S.W. and Wilson, R.

Genome Survey sequences from the parasitic nematode Ancylostoma

caninum

Unpublished (2004)

Contact: Mitreva M

Washington University in St. Louis

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjnhgwmc.edu) DNA
sequenced by Washington University Genome Sequencing Center
Class: shotgun.

FEATURES

Location/Qualifiers

```
1..845
/organism="Ancylostoma caninum"
/mol_type="genomic DNA"
/strain="Baltimore"
/db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
/clone_lib="Ancylostoma caninum whole genome shotgun
library (AIAAGSS 001)"
/note="Vector: pOTW13; Site 1: BstX1; Site 2: BstX1;
Ancylostoma caninum genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mtmjnhgwmc.edu) at George Washington University.
Sequencing by Washington University Genome Sequencing
Center, St. Louis, MO."
```

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 645;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20

Db 317 TTCAATGAGCTTCCTGAGCTT 298

RESULT 10

CC510758/c

LOCUS CH240_354A12.T7 CHORI-240 Bos taurus genomic clone CH240_354A12,
genomic survey sequence.

ACCESSION CC510758

VERSION CC510758.1 GI:31829046

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

REFERENCE

AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_354A12.TARBAC13P2
Contact: Rob Holt

TITLE

JOURNAL The British Columbia Cancer Agency Genome Science Centre
COMMENT 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.html>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 354 row: A column: 12
Seq primer: T7

Class: BAC ends.

FEATURES

Location/Qualifiers

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1..661
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_354A12"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
```

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 661;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20

Db 128 TCCAGGAGCTTCCTGAGCTT 109

RESULT 11

BH120643

LOCUS

PC1-24-288J21.TV RPCI-24 Mus musculus genomic clone
RPCI-24-288J21, genomic survey sequence.

ACCESSION BH120643

VERSION BH120643.1 GI:14964155

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 854)

AUTHORS

Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartabeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)

TITLE

JOURNAL Other GSSs: RPCI-24-288J21.TJ

COMMENT

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end
page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 288 row: J column: 21
Seq primer: T7

Class: BAC ends.

FEATURES

Location/Qualifiers

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1..854
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-288J21"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"

```

/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN
Query Match 92.0%; Score 18.4; DB 9; Length 854;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGAGCTTCCTGAGCTT 20
|||||
Db 835 TCATGAGCTTCCTGAGCTT 854

RESULT 12
BH640052/c
LOCUS
DEFINITION
202 bp DNA linear GSS 14-FEB-2002
survey sequence.

ACCESSION
BH640052
VERSION
BH640052.1 GI:18665976

KEYWORDS
GSS.

SOURCE
Zea mays

ORGANISM
Zea mays

REFERENCE
1 (bases 1 to 202)

AUTHORS
Walbot, V.

TITLE
Maize genomic sequences found using engineered RescueMu transposon

JOURNAL
Unpublished (2001)

COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1008033 row: 34
Class: transposon-tagged.
Location/Qualifiers
1..202

FEATURES
source

1..202

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1008 - RescueMu Grid I"

/notes="Organ: leaf; Vector: RescueMu (engineered from

phagescript backbone); Site1: BamHI; Site2: BglII;

RescueMu is a 4.9 Kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site www.zmbl.berkeley.edu and follow the links for

'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was

extracted from leaf punches, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 202;

Best Local Similarity 94.7%; Pred. No. 3.1e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

BU097976/c

LOCUS

DEFINITION

298 bp mRNA linear EST 29-AUG-2002

46122G05.y1 946 - tassell primordium prepared by Schmidt lab Zea

mays cDNA, mRNA sequence.

ACCESSION

BU097976

VERSION

BU097976.1 GI:22545617

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

REFERENCE

1 (bases 1 to 298)

AUTHORS

Walbot, V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

CONTACT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946122 row: G column: 05.

Location/Qualifiers

1..298

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue_type="tassels"

/dev_stage="just after the transition from vegetative to

inflorescence development"

/lab_host="XL0LR"

/clone_lib="946 - tassell primordium prepared by Schmidt

lab"

/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;

Site_2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybriZAP. Sample insert size range was 350 bp

to 3 Kb with a 1 Kb average."

ORIGIN

Query Match 87.0%; Score 17.4; DB 5; Length 298;

Best Local Similarity 94.7%; Pred. No. 3.2e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCCTGAGCTT 20

|||||

Db 101 CCATGAGCTTCCTGAGCTT 83

|||||

RESULT 14

CC096512/c

LOCUS

DEFINITION

316 bp DNA linear GSS 16-APR-2003

CSU-K34.113F11.T7 CSU-K34 Aedes aegypti genomic clone

CSU-K34.113F11, genomic survey sequence.

ACCESSION

CC096512

VERSION

CC096512.1 GI:29960084

KEYWORDS

GSS.

SOURCE

Aedes aegypti (yellow fever mosquito)

ORGANISM

Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Culicinae; Culicini; Aedes; Stegomyia.

1 (bases 1 to 316)

AUTHORS

Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.

TITLE

End sequencing of Aedes aegypti BACs

JOURNAL

Unpublished (2003)

COMMENT

Other_GSSs: CSU-K34.113F11.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

Department of Eukaryotic Genomics

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: entsa@tigr.org
 Library was provided by Susan Brown and Dennis Knudson at Colorado State University.
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1..316
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /db_xref="taxon:7159"
 /clone="CSU-K34.113F11"
 /clone_lib="CSU-K34"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Source DNA: Aedes aegypti; strain unknown (derived from freshly hatched larvae at the Virus Research Centre, Poona, India. Reference: SINGH, K. R. P., 1967 Cell cultures derived from larvae of Aedes albopictus (Skuse) and Aedes aegypti (L.). Current Science 36: 506-508]; ATC-10 cell line ATCC CCL-125"

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 316;
 Best Local Similarity 94.7%; Pred. No. 3.3e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCCTGAGCTT 20
 ||| |||||
 DB 102 CCAGGAGCTTCCTGAGCTT 84

RESULT 15

DE127737/c
 LOCUS DE127737 367 bp DNA linear GSS 02-AUG-2005
 DEFINITION Oryzias latipes DNA, reverse end of BAC clone: Md0178K15, genomic survey sequence.
 ACCESSION DE127737
 VERSION DE127737.1 GI:71622482
 KEYWORDS GSS.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 REFERENCE 1 Shimizu,N., Asakawa,S., Shimizu,A. and Sasaki,T.
 The BAC end sequence of Oryzias latipes
 TITLE Published Only in Database (2005)
 JOURNAL 2 (bases 1 to 367)
 REFERENCE Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.
 Direct Submission
 TITLE Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo, 160-8502, Japan (E-mail:nshimizu@mb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
 FEATURES
 source
 1..367
 /organism="Oryzias latipes"
 /mol_type="genomic DNA"
 /db_xref="taxon:8090"
 /clone="Md0178K15"
 /clone_lib="Medaka HdrR BAC library"
 /note="This sequence is reverse end of BAC clone Md0178K15."

ORIGIN

Query Match 87.0%; Score 17.4; DB 11; Length 367;
 Best Local Similarity 94.7%; Pred. No. 3.3e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCT 19
 |||||
 DB 100 TCCATGAGCTTCCTGCT 82
 Search completed: May 4, 2006, 07:17:35
 Job time : 1422.59 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 42.2989 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-5

Perfect score: 20
Sequence: 1 tccatgagcttctgagctt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/1 COMB.seq:*

2: /cgn2_6/prodata/1/ina/5 COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B COMB.seq:*

5: /cgn2_6/prodata/1/ina/H COMB.seq:*

6: /cgn2_6/prodata/1/ina/PCUS COMB.seq:*

7: /cgn2_6/prodata/1/ina/PP COMB.seq:*

8: /cgn2_6/prodata/1/ina/RE COMB.seq:*

9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	37335	3	US-09-949-016-17132
2	17	85.0	20	3	US-08-738-652-8
3	17	85.0	20	3	US-09-030-701-58
4	17	85.0	20	3	US-09-286-098-103
5	17	85.0	20	3	US-08-960-774-8
6	17	85.0	20	3	US-09-191-170-98
7	17	85.0	20	3	US-09-337-619-8
8	17	85.0	21	3	US-08-738-652-11
9	17	85.0	21	3	US-08-960-774-11
10	17	85.0	21	3	US-09-337-619-11
11	16.8	84.0	519	3	US-09-252-991A-6243
12	16.8	84.0	1131	3	US-09-252-991A-6329
C 13	16.8	84.0	1536	3	US-09-252-991A-6218
C 14	16.8	84.0	2077	3	US-10-104-047-1221
C 15	16.8	84.0	4494	3	US-09-566-921-55
C 16	16.8	84.0	45887	3	US-09-949-016-15936
C 17	16.4	82.0	601	3	US-09-949-016-148267
18	16.4	82.0	677	3	US-09-533-559-7185
C 19	16.4	82.0	719	3	US-09-533-559-5921
20	16.4	82.0	4113	3	US-09-799-451-532
C 21	16.4	82.0	23174	3	US-09-949-016-14387
C 22	16.4	82.0	23187	3	US-09-949-016-12235
C 23	16.4	82.0	42894	3	US-09-949-016-12301
C 24	16.4	82.0	42898	3	US-09-949-016-15904

25	16.4	82.0	105413	3	US-10-427-923-3	Sequence 3, Appli
26	16.4	82.0	112219	3	US-09-949-016-12453	Sequence 12453, A
27	16.4	82.0	112222	3	US-09-949-016-12424	Sequence 14324, A
28	16.4	82.0	113186	3	US-09-949-016-17572	Sequence 17572, A
29	16	80.0	20	3	US-09-082-649B-70	Sequence 70, Appl
30	16	80.0	20	3	US-09-965-101-70	Sequence 70, Appl
31	16	80.0	20	3	US-09-954-987B-85	Sequence 85, Appl
32	16	80.0	29	3	US-08-848-229-3	Sequence 3, Appli
C 33	16	80.0	29	3	US-09-022-965-3	Sequence 3, Appli
C 34	16	80.0	411	3	US-09-513-999C-9582	Sequence 9582, Ap
C 35	16	80.0	411	3	US-09-471-276-661	Sequence 661, App
36	16	80.0	23311	3	US-09-949-016-12344	Sequence 12344, A
37	16	80.0	23312	3	US-09-949-016-17217	Sequence 17217, A
38	16	80.0	33821	3	US-09-949-002-613	Sequence 613, App
39	16	80.0	33822	3	US-09-949-002-737	Sequence 737, App
40	16	80.0	33827	3	US-09-949-002-760	Sequence 760, App
C 41	15.8	79.0	462	3	US-09-252-991A-5265	Sequence 5265, Ap
C 42	15.8	79.0	522	3	US-09-614-912-53	Sequence 53, Appl
C 43	15.8	79.0	601	3	US-09-949-016-113758	Sequence 113758, A
C 44	15.8	79.0	601	3	US-09-949-016-113926	Sequence 113926, A
C 45	15.8	79.0	601	3	US-09-949-016-114094	Sequence 114094, A

ALIGNMENTS

RESULT 1
US-09-949-016-17132/c
; Sequence 17132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17132
; LENGTH: 37335
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17132

Query Match 87.0%; Score 17.4; DB 3; Length 37335;
Best Local Similarity 94.7%; Pred No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTGAGCTT 20
|||||
Db 29042 CCATGAGTTCTGAGCTT 29024

RESULT 2
US-08-738-652-8
; Sequence 8, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063

; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-8

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
|||||
DB 1 TCCATGAGCTTCCTGAG 17

RESULT 3
US-09-030-701-58
; Sequence 58, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-58

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
|||||
DB 1 TCCATGAGCTTCCTGAG 17

RESULT 4
US-09-286-098-103
; Sequence 103, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-103

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
|||||
DB 1 TCCATGAGCTTCCTGAG 17

RESULT 5
US-08-960-774-8
; Sequence 8, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-960-774-8

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
|||||
DB 1 TCCATGAGCTTCCTGAG 17

RESULT 6
US-09-191-170-98
; Sequence 98, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-98

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 7

US-09-337-619-8
; Sequence 8, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; EARLIER FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-337-619-8

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 8

US-08-738-652-11
; Sequence 11, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-11

Query Match 85.0%; Score 17; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 9
US-08-960-774-11
; Sequence 11, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
US-08-960-774-11

Query Match      85.0%; Score 17; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
   |||||
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 10
US-09-337-619-11
; Sequence 11, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; PRIOR FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-11

Query Match      85.0%; Score 17; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
   |||||
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 11
US-09-252-991A-6243
; Sequence 6243, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6243
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6243

Query Match      84.0%; Score 16.8; DB 3; Length 519;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
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Db 1 TCCATGAGCTTCATGAACCTT 1067

RESULT 12
US-09-252-991A-6329
; Sequence 6329, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6329
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6329

Query Match      84.0%; Score 16.8; DB 3; Length 1131;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
   |||||
Db 1 TCCATGAGCTTCATGAACCTT 20

RESULT 13
US-09-252-991A-6218/c
; Sequence 6218, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6218
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6218

Query Match      84.0%; Score 16.8; DB 3; Length 1536;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
   |||||
Db 1086 TCCATGAGCTTCATGAACCTT 1067

RESULT 14
US-10-104-047-1221/c
; Sequence 1221, Application US/10104047
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; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1221
; LENGTH: 2077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1221

Query Match 84.0%; Score 16.8; DB 3; Length 2077;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 428 TCCATGAGCTTCCTGAGCTT 409

RESULT 15
US-09-566-921-55/c
; Sequence 55, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 55
; LENGTH: 4494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 024844.5
US-09-566-921-55

Query Match 84.0%; Score 16.8; DB 3; Length 4494;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1486 TCCATGAGCTTCCTGAGCTT 1467

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Job time : 44.2989 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 07:24:16 ; Search time 298.851 Seconds
(without alignments)
553.412 Million cell updates/sec

Title: US-10-789-758A-5
Perfect score: 20
Sequence: 1 tccatgagcttcctgagctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-768-012-2
2	20	100.0	20	3	US-09-888-326-573
3	20	100.0	20	3	US-09-776-479-887
4	20	100.0	20	3	US-09-776-479-887
5	20	100.0	20	5	US-10-112-653-858
6	20	100.0	20	5	US-10-017-995-887
7	20	100.0	20	6	US-10-314-578-887
8	20	100.0	20	8	US-10-831-778-887
9	20	100.0	20	8	US-10-789-758-5
10	18.4	92.0	312477	7	US-10-317-883A-12
11	17.4	87.0	694	7	US-10-424-599-17537
12	17.4	87.0	2394	7	US-10-437-963-40847
13	17.4	87.0	2616	8	US-10-739-930-1939
14	17	85.0	20	3	US-09-824-468-103
15	17	85.0	20	3	US-09-888-326-574
16	17	85.0	20	3	US-09-888-326-575
17	17	85.0	20	3	US-09-888-326-576
18	17	85.0	20	3	US-09-818-918-8
19	17	85.0	20	3	US-09-776-479-27
20	17	85.0	20	3	US-09-776-479-92
21	17	85.0	20	3	US-09-776-479-200
22	17	85.0	20	3	US-09-776-479-871
23	17	85.0	20	3	US-09-776-479-27

24	17	85.0	20	3	US-09-776-479-92	Sequence 92, Appl
25	17	85.0	20	3	US-09-776-479-200	Sequence 200, App
26	17	85.0	20	3	US-09-776-479-871	Sequence 871, App
27	17	85.0	20	5	US-10-112-653-27	Sequence 27, Appl
28	17	85.0	20	5	US-10-112-653-193	Sequence 193, App
29	17	85.0	20	5	US-10-112-653-842	Sequence 842, App
30	17	85.0	20	5	US-10-017-995-27	Sequence 27, Appl
31	17	85.0	20	5	US-10-017-995-92	Sequence 92, Appl
32	17	85.0	20	5	US-10-017-995-200	Sequence 200, App
33	17	85.0	20	5	US-10-017-995-871	Sequence 871, App
34	17	85.0	20	5	US-10-161-229-98	Sequence 98, Appl
35	17	85.0	20	6	US-10-187-264A-8	Sequence 8, Appli
36	17	85.0	20	6	US-10-306-522-8	Sequence 8, Appli
37	17	85.0	20	6	US-10-314-578-27	Sequence 27, Appl
38	17	85.0	20	6	US-10-314-578-92	Sequence 92, Appl
39	17	85.0	20	6	US-10-314-578-200	Sequence 200, App
40	17	85.0	20	6	US-10-314-578-871	Sequence 871, App
41	17	85.0	20	7	US-10-719-493-8	Sequence 8, Appli
42	17	85.0	20	7	US-10-627-331-8	Sequence 8, Appli
43	17	85.0	20	7	US-10-743-625-8	Sequence 8, Appli
44	17	85.0	20	7	US-10-679-710-8	Sequence 8, Appli
45	17	85.0	20	7	US-10-769-282-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-768-012-2
; Sequence 2, Application US/09768012
; Patent No. US20010044416A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: McCluskie, Michael J.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for
; TITLE OF INVENTION: Inducing a Th2 Immune Response
; FILE REFERENCE: C10407/7010/HCL/MAT
; CURRENT APPLICATION NUMBER: US/09/768,012
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,461
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-768-012-2

Query Match 100.0% Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 TCCATGAGCTTCCTGAGCTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 2
US-09-888-326-573
; Sequence 573, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346

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/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 887
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-887

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
Db 1 TCCATGAGCTTCCTGAGCTT 20
    |||||

RESULT 5
US-10-112-653-858
/ Sequence 858, Application US/10112653
/ Publication No. US20030050268A1
/ GENERAL INFORMATION:
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Berg, Daniel J.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
/ TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
/ FILE REFERENCE: C01039/70060(AWS)
/ CURRENT APPLICATION NUMBER: US/10/112,653
/ CURRENT FILING DATE: 2002-03-29
/ PRIOR APPLICATION NUMBER: US 60/279,642
/ PRIOR FILING DATE: 2001-03-29
/ NUMBER OF SEQ ID NOS: 1040
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 858
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-858

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
Db 1 TCCATGAGCTTCCTGAGCTT 20
    |||||

RESULT 6
US-10-017-995-887
/ Sequence 887, Application US/10017995
/ Publication No. US20030055014A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
/ FILE REFERENCE: C1037/7025 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/10/017,995
/ CURRENT FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: US 60/255,534
/ PRIOR FILING DATE: 2000-12-14
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 887
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-10-017-995-887
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/ PRIOR FILING DATE: 2000-06-22
/ NUMBER OF SEQ ID NOS: 848
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 573
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide
/ NAME/KEY: misc feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-573

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
Db 1 TCCATGAGCTTCCTGAGCTT 20
    |||||

RESULT 3
US-09-776-479-887
/ Sequence 887, Application US/09776479
/ Publication No. US20030087848A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fournon, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ TITLE OF INVENTION: Treatment of Asthma and Allergy
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 887
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-887

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
    |||||
Db 1 TCCATGAGCTTCCTGAGCTT 20
    |||||

RESULT 4
US-09-776-479-887
/ Sequence 887, Application US/09776479
/ Publication No. US20040067902A9
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fournon, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ TITLE OF INVENTION: Treatment of Asthma and Allergy
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
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Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 7

US-10-314-578-887
; Sequence 887, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-887

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 8

US-10-831-778-887
; Sequence 887, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-887

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 9

US-10-789-758-5
; Sequence 5, Application US/10789758
; Publication No. US20050002958A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Joe
; APPLICANT: Garcon, Nathalie
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45187
; CURRENT APPLICATION NUMBER: US/10/789,758
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/018,704
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/EP00/05841
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: GB 9915204.3
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing a GpC motif
US-10-789-758-5

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20
|||||
Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 10

US-10-317-883A-12
; Sequence 12, Application US/10317883A
; Publication No. US20040115641A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ROCK 1 EXPRESSION
; FILE REFERENCE: RTS-0438
; CURRENT APPLICATION NUMBER: US/10/317,883A
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 12
; LENGTH: 312477
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31186-31258
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 39181
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 39183
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:

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/ NAME/KEY: misc_feature
/ LOCATION: 39464-39563
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 51426-51525
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 56648
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 56710-56809
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 65039-65138
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 73415-73514
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 79644-79743
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 86851-86950
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 92371-92470
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 97243-97342
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 102609-102708
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 106849-106948
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 113142-113241
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 117089-117188
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 121444-121543
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 126722-126721
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 130441-130541
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 135160-135259
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 135692
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 138860-138959
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 141856-141955
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 144205-144304
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 146475-146574
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 147608-147707
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 149158-149257
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 160337-160436
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 193431-193530
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 204369
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 227937
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 227963-228062
/ OTHER INFORMATION: n = A,T,C or G
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/ LOCATION: 243193-243292
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 245887-245986
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 263803-263902
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 266516-266645
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 267821-267920
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 275949-276048
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 280464
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OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 280587
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 281830
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 281920
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 281923
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 282024
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 282032
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature

Query Match 92.0%; Score 18.4; DB 7; Length 312477;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCGAGCTT 20
|||||
Db 184253 TCCATGAGCTTCTGATCTT 184272

RESULT 11
US-10-424-599-17537
; Sequence 17537, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 17537
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(694)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115840C.1
US-10-424-599-17537

Query Match 87.0%; Score 17.4; DB 7; Length 694;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCGAGCTT 20
|||||
Db 367 TCCATGAGCTTGCGAGCTT 386

RESULT 12
US-10-437-963-40847/c
; Sequence 40847, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 40847
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2394)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44249C.1
US-10-437-963-40847

Query Match 87.0%; Score 17.4; DB 7; Length 2394;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTGAGCTT 20
|||||
Db 103 CCATGAGCTTCTGAGCTT 85

RESULT 13
US-10-739-930-1939/c
; Sequence 1939, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 1939
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-CLUSTER16551_3
US-10-739-930-1939

Query Match 87.0%; Score 17.4; DB 8; Length 2616;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCATGAGCTTCTGAGCTT 20
|||||
Db 312 CCATGAGCTTCTGAGCTT 294

RESULT 14
US-09-824-468-103
; Sequence 103, Application US/09824468
; Patent No. US20020064515A1

GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/824,468
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/286,098
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 103
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-824-468-103

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
DB 1 TCCATGAGCTTCCTGAG 17

RESULT 15
US-09-888-326-574
Sequence 574, Application US/09888326
Publication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 574
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: phosphodiester backbone
US-09-888-326-574

Query Match 85.0%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
DB 1 TCCATGAGCTTCCTGAG 17

Search completed: May 4, 2006, 09:01:05
Job time : 300.851 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 08:17:52 ; Search time 456.437 Seconds
(without alignments)
178.449 Million cell updates/sec

Title: US-10-789-758A-5

Perfect score: 20

Sequence: 1 tccatgagcttcctgagctt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New*

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 7: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 8: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 15: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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- 18: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 19: /SIDSS/ptodata/2/pubpna/US16_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	17	US-11-127-654-858
2	17	85.0	20	10	US-10-619-279-8
3	17	85.0	20	10	US-10-435-656-8
4	17	85.0	20	12	US-10-382-822-8
5	17	85.0	20	14	US-11-296-572-8
6	17	85.0	20	17	US-11-127-654-27
7	17	85.0	20	17	US-11-127-654-193
8	17	85.0	20	17	US-11-127-654-842
9	17	85.0	20	17	US-11-134-918-8
10	17	85.0	20	17	US-11-031-460-8
11	17	85.0	20	17	US-11-067-587-8
12	17	85.0	20	17	US-11-099-683-82
13	17	85.0	21	10	US-10-619-279-11
14	17	85.0	21	10	US-10-435-656-11

15	17	85.0	21	12	US-10-382-822-11	Sequence 11, Appl
16	17	85.0	21	14	US-11-296-572-11	Sequence 11, Appl
17	17	85.0	21	17	US-11-134-918-11	Sequence 11, Appl
18	17	85.0	21	17	US-11-031-460-11	Sequence 11, Appl
19	17	85.0	21	17	US-11-067-587-11	Sequence 11, Appl
20	16.8	84.0	600	10	US-10-750-185-570	Sequence 570, App
21	16.8	84.0	600	10	US-10-750-623-570	Sequence 570, App
C 22	16.8	84.0	642	7	US-09-925-065A-747839	Sequence 747839,
C 23	16.8	84.0	667	7	US-09-925-065A-821205	Sequence 821205,
C 24	16.8	84.0	678	11	US-10-301-480-100187	Sequence 100187,
C 25	16.8	84.0	678	12	US-10-301-480-713596	Sequence 713596,
C 26	16.8	84.0	703	13	US-10-960-414-65	Sequence 65, Appl
C 27	16.8	84.0	2077	18	US-11-072-512-1221	Sequence 1221, Ap
C 28	16.8	84.0	2338	17	US-11-136-537-2898	Sequence 2898, Ap
C 29	16.8	84.0	3219	11	US-10-932-182A-82170	Sequence 82170, A
C 30	16.8	84.0	3219	11	US-10-932-182A-82170	Sequence 82170, A
C 31	16.4	82.0	572	7	US-09-925-065A-90026	Sequence 90026, A
C 32	16.4	82.0	572	7	US-09-925-065A-90027	Sequence 90027, A
C 33	16.4	82.0	572	7	US-09-925-065A-90028	Sequence 90028, A
C 34	16.4	82.0	572	11	US-10-301-480-191267	Sequence 191267,
C 35	16.4	82.0	572	11	US-10-301-480-191268	Sequence 191268,
C 36	16.4	82.0	572	11	US-10-301-480-191269	Sequence 191269,
C 37	16.4	82.0	572	12	US-10-301-480-804676	Sequence 804676,
C 38	16.4	82.0	572	12	US-10-301-480-804677	Sequence 804677,
C 39	16.4	82.0	572	12	US-10-301-480-804678	Sequence 804678,
C 40	16.4	82.0	575	7	US-09-925-065A-751057	Sequence 751057,
C 41	16.4	82.0	600	17	US-11-128-061-6840	Sequence 6840, Ap
C 42	16.4	82.0	600	17	US-11-128-049-6840	Sequence 6840, Ap
C 43	16.4	82.0	619	11	US-10-301-480-29145	Sequence 29145, A
C 44	16.4	82.0	619	11	US-10-301-480-29146	Sequence 29146, A
C 45	16.4	82.0	619	12	US-10-301-480-842554	Sequence 842554,

ALIGNMENTS

RESULT 1

US-11-127-654-858

Sequence 858, Application US/11127654

Publication No. US20050250726A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

FILE REFERENCE: C1039.70060U01

FILE REFERENCE: INFLAMMATORY DISEASES

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/112,653

PRIOR FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: US 60/279,642

NUMBER OF SEQ ID NOS: 1040

SOFTWARE: PatentIn version 3.2

SEQ ID NO 858

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide

US-11-127-654-858

Query Match 100.0%; Score 20; DB 17; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAGCTT 20

Db 1 TCCATGAGCTTCCTGAGCTT 20

RESULT 2

US-10-619-279-8

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; Sequence 8, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-8
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Query Match      85.0%; Score 17; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17
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RESULT 3
US-10-435-656-8
; Sequence 8, Application US/10435656
; Publication No. US20050277604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-8
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Query Match      85.0%; Score 17; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17
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RESULT 4
US-10-382-822-8
; Sequence 8, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; FILE REFERENCE: C01039.70062.US
; CURRENT APPLICATION NUMBER: US/10/382,822
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-382-822-8
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Query Match      85.0%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TCCATGAGCTTCCTGAG 17
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 5
US-11-296-572-8
; Sequence 8, Application US/11296572
; Publication No. US20060089326A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/296,572
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-296-572-8
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Query Match      85.0%; Score 17; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
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Db 1 TCCATGAGCTTCCTGAG 17

RESULT 6
US-11-127-654-27
; Sequence 27, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US 11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-27

Query Match      85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
   |||||
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 7
US-11-127-654-193
; Sequence 193, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US 11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-193

Query Match      85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TCCATGAGCTTCCTGAG 17
   |||||
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 8
US-11-127-654-842
; Sequence 842, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US 11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 842
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-842

Query Match      85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCCTGAG 17
   |||||
Db 1 TCCATGAGCTTCCTGAG 17

RESULT 9
US-11-134-918-8
; Sequence 8, Application US/11134918
; Publication No. US20050267064A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US 11/134,918
; CURRENT FILING DATE: 2005-05-23
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-134-918-8

Query Match      85.0%; Score 17; DB 17; Length 20;
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Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAG 17
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Db 1 TCCATGAGCTTCTCTGAG 17

RESULT 10
US-11-031-460-8
; Sequence 8, Application US/11031460
; Publication No. US20050277609A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/031,460
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-031-460-8

Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAG 17
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Db 1 TCCATGAGCTTCTCTGAG 17

RESULT 11
US-11-067-587-8
; Sequence 8, Application US/11067587
; Publication No. US2006003955A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/067,587
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-067-587-8

Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAG 17
   |||||
Db 1 TCCATGAGCTTCTCTGAG 17

RESULT 12
US-11-099-683-82
; Sequence 82, Application US/11099683
; Publication No. US20060019916A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
; FILE REFERENCE: C1037.70047US01
; CURRENT APPLICATION NUMBER: US/11/099,683
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/558,951
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-099-683-82

Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGAGCTTCTCTGAG 17
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Db 1 TCCATGAGCTTCTCTGAG 17

RESULT 13
US-10-619-279-11
; Sequence 11, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-11
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US-10-619-279-11

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Query Match      85.0%; Score 17; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  TCCATGAGCTTCCTCGAG 17

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RESULT 14

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US-10-435-656-11
; Sequence 11, Application US/10435656
; Publication No. US20050277604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-11

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Query Match      85.0%; Score 17; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCTCTGAG 17
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Db 1 TCCATGAGCTTCTCTGAG 17
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RESULT 15

US-10-382-022-11
; Sequence 11, Application US/1038282
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; TITLE OF INVENTION: Infectious Disease
; FILE REFERENCE: C01039.70062 US
; CURRENT APPLICATION NUMBER: US/10/382,822
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 02:22:43 ; Search time 464.368 Seconds
(without alignments)
2448.208 Million cell updates/sec

Title: US-10-789-758A-6

Perfect score: 20
Sequence: 1 tccatgacgttctctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_env.*
4: gb_om.*
5: gb_ov.*
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8: gb_pr.*
9: gb_ro.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	20	100.0	20	6	AR146388 Sequence
4	20	100.0	20	6	AR146393 Sequence
5	20	100.0	20	6	AR154681 Sequence
6	20	100.0	20	6	BD069973 Use of nu
7	20	100.0	20	6	BD190417 Microemul
8	20	100.0	20	6	BD205610 Method of
9	20	100.0	20	6	BD205615 Method of
10	20	100.0	20	6	BD222610 Compositi
11	20	100.0	20	6	BD251265 Enhanceme
12	20	100.0	20	6	BD261152 Methods a
13	20	100.0	20	6	BD261157 Methods a
14	20	100.0	20	6	BD261307 Methods a
15	20	100.0	20	6	BD261311 Methods a
16	20	100.0	20	6	BD261560 Vaccine
17	20	100.0	20	6	BD267913 Methods f
18	20	100.0	20	6	BD270813 Stereoiso

19	20	100.0	20	6	BD270817	Stereoiso
20	20	100.0	20	6	CQ753470	Sequence
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22	20	100.0	20	6	CQ769069	Sequence
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40	20	100.0	20	6	CS057843	Sequence
41	20	100.0	20	6	CS083013	Sequence
42	20	100.0	20	6	CS086355	Sequence
43	20	100.0	20	6	CS088751	Sequence
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ALIGNMENTS

RESULT 1
AR078395
LOCUS AR078395
DEFINITION Sequence 12 from patent US 5962636.
ACCESSION AR078395
VERSION AR078395.1 GI:10005141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bachmaier,K., Hessel,A.John., Neu,N. and Penninger,J.Martin.
TITLE Peptides capable of modulating inflammatory heart disease
JOURNAL Patent: US 5962636-A 12 05-OCT-1999;
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Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20
RESULT 2
AR140451
LOCUS AR140451
DEFINITION Sequence 10 from patent US 6207646.
ACCESSION AR140451
VERSION AR140451.1 GI:14482947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.

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TITLE      Immunostimulatory nucleic acid molecules
JOURNAL    Patent: US 6207646-A 10 27-MAR-2001;
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    Location/Qualifiers
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      /mol_type="unassigned DNA"
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
RESULT 3
LOCUS      AR146388
DEFINITION Sequence 100 from patent US 6218371.
ACCESSION  AR146388
VERSION     AR146388.1 GI:15109577
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Krieg,A.M. and Weiner,G.
TITLE     Methods and products for stimulating the immune system using
          immunotherapeutic oligonucleotides and cytokines
JOURNAL    Patent: US 6218371-A 10 17-APR-2001;
FEATURES
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    Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
RESULT 4
LOCUS      AR146393
DEFINITION Sequence 105 from patent US 6218371.
ACCESSION  AR146393
VERSION     AR146393.1 GI:15109582
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Krieg,A.M. and Weiner,G.
TITLE     Methods and products for stimulating the immune system using
          immunotherapeutic oligonucleotides and cytokines
JOURNAL    Patent: US 6218371-A 10 17-APR-2001;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
TITLE      Immunostimulatory nucleic acid molecules
JOURNAL    Patent: US 6207646-A 10 27-MAR-2001;
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
RESULT 5
LOCUS      AR154681
DEFINITION Sequence 10 from patent US 6239116.
ACCESSION  AR154681
VERSION     AR154681.1 GI:15122734
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Krieg,A.M. and Kline,J.N.
TITLE     Immunostimulatory nucleic acid molecules
          Patent: US 6239116-A 10 29-MAY-2001;
JOURNAL    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 18;
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QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
RESULT 6
LOCUS      BD069973
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
          the treatment of LPS-associated disorders.
ACCESSION  BD069973
VERSION     BD069973.1 GI:22615576
KEYWORDS   JP 2001513776-A/62.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Schwartz,D.A. and Krieg,A.M.
TITLE     Use of nucleic acids containing unmethylated CPG dinucleotide in
          the treatment of LPS-associated disorders
JOURNAL    Patent: JP 2001513776-A 62 04-SEP-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT    OS Artificial Sequence
          PN JP 2001513776-A/62
          PD 04-SEP-2001
          PF 25-FEB-1998 JP 1998537810
          PI 28-FEB-1997 US 60/039405
          PR DAVID A SCHWARTZ, ARTHUR M KRIEG
          PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
          CC Synthetic oligonucleotide
          FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCCATGACGTTCTCTGACGTT 20
Db      1 TCCATGACGTTCTCTGACGTT 20
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Db      1  TCCATGACGTTCTCTGACGTT 20
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RESULT 7
BD190417          20 bp  DNA  linear  PAT 17-JUL-2003
LOCUS             Microemulsions with Adsorbed Macromolecules and Microparticles.
DEFINITION
ACCESSION  BD190417
VERSION    BD190417.1  GI:330000156
KEYWORDS   JP 2002537102-A/1.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,
            Ott,G.S. and Ohagan,D.
TITLE       Microemulsions with Adsorbed Macromolecules and Microparticles
JOURNAL     Patent: JP 2002537102-A 1 05-NOV-2002;
            Chiron Corporation
COMMENT     OS  Artificial Sequence
            PN  JP 2002537102-A/1
            PD  05-NOV-2002
            PP  09-FEB-2000  JP 2000600618
            PR  23-JUL-1999  US  60/146391,28-OCT-1999  US  60/161997, PR
            26-FEB-1999  US  60/121858
            PI  John Barackman,manmohan simph,mildred ugozoli,jina kazazu,john
            Donnelly,
            PI  Gary a ott,derek ohagan
            CC  Oligonucleotide
            FH  Key  Location/Qualifiers
                1. .20
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20
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RESULT 8
BD205610
LOCUS             20 bp  DNA  linear  PAT 17-JUL-2003
DEFINITION
ACCESSION  BD205610
VERSION    BD205610.1  GI:33015380
KEYWORDS   JP 2002514397-A/100.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Wagner,H. and Lipford,G.
TITLE       Method of controlling hematopoiesis by using CpG oligonucleotide
JOURNAL     Patent: JP 2002514397-A 100 21-MAY-2002;
            CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC
COMMENT     OS  Artificial Sequence
            PN  JP 2002514397-A/100
            PD  21-MAY-2002
            PP  14-MAY-1998  JP 2000547969
            PR  14-MAY-1998  US  60/085516,02-FEB-1999  US  09/241653 PI
            PC  C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00
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FEATURES             source
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20
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RESULT 9
BD205615
LOCUS             20 bp  DNA  linear  PAT 17-JUL-2003
DEFINITION
ACCESSION  BD205615
VERSION    BD205615.1  GI:33015385
KEYWORDS   JP 2002514397-A/105.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Wagner,H. and Lipford,G.
TITLE       Method of controlling hematopoiesis by using CpG oligonucleotide
JOURNAL     Patent: JP 2002514397-A 105 21-MAY-2002;
            CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC
COMMENT     OS  Artificial Sequence
            PN  JP 2002514397-A/105
            PD  21-MAY-2002
            PP  14-MAY-1998  JP 2000547969
            PR  14-MAY-1998  US  60/085516,02-FEB-1999  US  09/241653 PI
            PC  C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00
            CC  Synthetic Sequence
            FH  Key  Location/Qualifiers
            FT  source 1. .20
FEATURES             source
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1  TCCATGACGTTCTCTGACGTT 20
Db      1  TCCATGACGTTCTCTGACGTT 20
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RESULT 10
BD222610
LOCUS             20 bp  DNA  linear  PAT 17-JUL-2003
DEFINITION
ACCESSION  BD222610
VERSION    BD222610.1  GI:33032380
KEYWORDS   JP 2002522510-A/2.
SOURCE     Quillaja saponaria
            Quillaja saponaria
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Quillajaceae; Quillaja.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Kensil,C.A.

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TITLE      Compositions of CPG and saponin adjuvants and uses thereof
JOURNAL    Patent: JP 2002522510-A 2 23-JUL-2002;
COMMENT    AQUILA BIOPHARMACEUTICALS INC
OS         Quillaaja saponaria
PN         JP 2002522510-A/2
PD         23-JUL-2002
PF         06-AUG-1999 JP 2000564661
PR         10-AUG-1999 US 60/095913,08-APR-1999 US 60/128608 PI
PC         CHARLOTTE A KENSIL
CC         A61K39/39,A61K39/00,C12N15/09,C12N15/00
CC         Compositions of CPG and saponin adjuvants and uses thereof FH
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   TCCATGACGTTCTCTGACGTT 20
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Db       1   TCCATGACGTTCTCTGACGTT 20

RESULT 11
BD251265      20 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Enhancement of Neisseria antigen bactericidal activity using CG
DEFINITION    motif-containing oligonucleotide.
ACCESSION     BD251265
VERSION       BD251265.1 GI:33061035
KEYWORDS      JP 2002537353-A/1.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 20)
AUTHORS       Grandi,G., Rappuoli,R., Giuliani,M.M. and Pizza,M.
TITLE         Enhancement of Neisseria antigen bactericidal activity using CG
JOURNAL       motif-containing oligonucleotide
COMMENT       Patent: JP 2002537353-A 1 05-NOV-2002;
              CHIRON SPA
OS         Artificial Sequence
PN         JP 2002537353-A/1
PD         05-NOV-2002
PF         09-FEB-2000 JP 2000600685
PR         26-FEB-1999 US 60/121792
PI         GUIDO GRANDI,RINO RAPPUOLI,MARZIA MONICA GIULIANI,MARIAGRAZIA
PI         PIZZA
PC         A61K39/095,A61K31/7088,A61K39/39,A61P31/04//CO7K14/22,C12N15/
PC         09,C12N15/00
CC         oligonucleotide adjuvant
CC         Location/Qualifiers
FH         Key
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FT         source
FT         /organism="Artificial Sequence".

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            /db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   TCCATGACGTTCTCTGACGTT 20
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Db       1   TCCATGACGTTCTCTGACGTT 20

RESULT 12
BD261152      20 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Methods and products for stimulating the immune system using
DEFINITION    immunotherapeutic oligonucleotides and cytokines.
ACCESSION     BD261152
VERSION       BD261152.1 GI:33070922
KEYWORDS      JP 2002510644-A/100.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 20)
AUTHORS       Krieg,A.M. and Weiner,G.
TITLE         Methods and products for stimulating the immune system using
JOURNAL       immunotherapeutic oligonucleotides and cytokines
JOURNAL       Patent: JP 2002510644-A 100 09-APR-2002;
              UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT       OS Artificial Sequence
              PN JP 2002510644-A/100
              PD 09-APR-2002
              PF 02-APR-1999 JP 2000542030
              PR 03-APR-1998 US 60/080729
              PI ARTHUR M KRIEG,GEORGE WEINER
              PC A61K38/00,A61K31/7088,A61K39/00,A61P15/00,A61P35/00,A61P37/04,
              PC A61K37/02
              CC Synthetic Sequence
              CC Key
              CC Location/Qualifiers
              FT source
              FT 1..20
              FT /organism="Artificial Sequence".

FEATURES   source
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   TCCATGACGTTCTCTGACGTT 20
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Db       1   TCCATGACGTTCTCTGACGTT 20

RESULT 13
BD261157      20 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Methods and products for stimulating the immune system using
DEFINITION    immunotherapeutic oligonucleotides and cytokines.
ACCESSION     BD261157
VERSION       BD261157.1 GI:33070927
KEYWORDS      JP 2002510644-A/105.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 20)
AUTHORS       Krieg,A.M. and Weiner,G.
TITLE         Methods and products for stimulating the immune system using
JOURNAL       immunotherapeutic oligonucleotides and cytokines
JOURNAL       Patent: JP 2002510644-A 105 09-APR-2002;
              UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT       OS Artificial Sequence
              PN JP 2002510644-A/105
              PD 09-APR-2002
              PF 02-APR-1999 JP 2000542030
              PR 03-APR-1998 US 60/080729
              PI ARTHUR M KRIEG,GEORGE WEINER
              PC A61K38/00,A61K31/7088,A61K39/00,A61P15/00,A61P35/00,A61P37/04,
              PC A61K37/02

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	2	AAV60950 Unmethyla
2	20	100.0	20	2	AAV47683 Unmethyla
3	20	100.0	20	2	AAV27667 Immunosti
4	20	100.0	20	2	AAZ41946 IL-12 sec
5	20	100.0	20	2	AAZ41949 IL-12 sec
6	20	100.0	20	2	AAx78802 HPV fusio
7	20	100.0	20	2	AAZ31943 CpG adjuv
8	20	100.0	20	2	AAV74237 CpG-N mot
9	20	100.0	20	2	AAV74244 CpG-N mot
10	20	100.0	20	2	AAV74242 CpG-N mot
11	20	100.0	20	2	AAx88536 Cytosine-
12	20	100.0	20	2	AAZ28191 Chlamydia-
13	20	100.0	20	3	AAZ61012 Nucleotid
14	20	100.0	20	3	AAZ61010 Nucleotid
15	20	100.0	20	3	AAZ48025 Immune re
16	20	100.0	20	3	AAZ48022 Immune re
17	20	100.0	20	3	AAZ47885 Immunosti
18	20	100.0	20	3	AAZ47887 Immunosti
19	20	100.0	20	3	AAA90447 CpG adjuv

20	20	100.0	20	3	AAZ99174	Aaz99174 Inflammat
21	20	100.0	20	3	AAZ99004	Aaz99004 CpG motif
22	20	100.0	20	3	AAZ47601	Aaz47601 Murine im
23	20	100.0	20	3	AAZ60277	Aaz60277 Immunosti
24	20	100.0	20	3	AAZ64136	Aaz64136 Immunosti
25	20	100.0	20	4	AAH20390	Aah20390 CpG motif
26	20	100.0	20	4	AAH20392	Aah20392 CpG motif
27	20	100.0	20	4	AAH50580	Aah50580 CpG motif
28	20	100.0	20	4	AAH19260	Aah19260 CpG oligo
29	20	100.0	20	4	AAAF98805	Aaf98805 CpG immun
30	20	100.0	20	4	AAAF59506	Aaf59506 Immunosti
31	20	100.0	20	4	AAAF59501	Aaf59501 Immunosti
32	20	100.0	20	4	AAAC82106	Aac82106 Oligonuel
33	20	100.0	20	4	AAAF99748	Aaf99748 Immunosti
34	20	100.0	20	4	AAAF99745	Aaf99745 Immunosti
35	20	100.0	20	4	AAAF98944	Aaf98944 Immunosti
36	20	100.0	20	4	AAAF99752	Aaf99752 Immunosti
37	20	100.0	20	4	AAAF99175	Aaf99175 Immunosti
38	20	100.0	20	4	AAAF99750	Aaf99750 Immunosti
39	20	100.0	20	4	AAAF99744	Aaf99744 Immunosti
40	20	100.0	20	4	AAAF99751	Aaf99751 Immunosti
41	20	100.0	20	4	AAAF99012	Aaf99012 Immunosti
42	20	100.0	20	4	AAAF99746	Aaf99746 Immunosti
43	20	100.0	20	4	AAAF99753	Aaf99753 Immunosti
44	20	100.0	20	4	AAAF99817	Aaf99817 Immunosti
45	20	100.0	20	4	AAAF99749	Aaf99749 Immunosti

ALIGNMENTS

RESULT 1

AAV60950
ID AAV60950 standard; DNA; 20 BP.

AC AAV60950;

DT 14-DEC-1998 (first entry)

DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
KW ss; unmethylated CpG dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.

OS Synthetic.

PN WO9840100-A1.

PD 17-SEP-1998.

PF 10-MAR-1998; 98WO-US004703.

PR 10-MAR-1997; 97US-0040376P.

PA (OTTA-) OTTAWA CIVIC LOBB RES INST.

(QIAG-) QIAGEN GMBH.

(IOWA) UNIV IOWA RES FOUND.

PI Davis HL, Schorr J, Krieg AM;

WPI; 1998-520792/44.

Use of oligonucleotides containing an unmethylated CpG dinucleotide -
useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
for inducing immune response in subject.

Claim 14; Page 35; 67pp; English.

Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
affect the immune response in a subject by activating natural killer
cells or redirecting a subject's immune response from a Th2 to a Th1
response by inducing monocytic and other cells to produce Th1 cytokines.
These nucleic acids containing at least 1 unmethylated CpG can be used as

CC an adjuvant, specifically to induce an immune response against an
 CC antigenic protein, and are used particularly for virally mediated
 CC disorders, e.g. hepatitis B virus infection

XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2

AAV47683
 ID AAV47683 standard; DNA; 20 BP.

XX AC AAV47683;

XX DT 20-NOV-1998 (first entry)

XX DE Unmethylated CpG dinucleotide 1826.

XX KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KW pulmonary disorder; asthma; environmentally induced airway disease;
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KW inflammatory bowel disease; ss.

XX OS Synthetic.

XX PN WO9837919-A1.

XX PD 03-SEP-1998.

XX PF 25-FEB-1998; 98WO-US003678.

XX PR 28-FEB-1997; 97US-0039405P.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PI Schwartz DA, Krieg AM;

XX PS WPI; 1998-480941/41.

XX PT Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow or
 PT inhibiting an inflammatory response.

XX PS Claim 35; Page 27; 65pp; English.

XX CC This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated CpG. The nucleic acid contains an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an
 CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with Gram-
 CC positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide

XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3

AAV27667

XX ID AAV27667 standard; DNA; 20 BP.

XX AC AAV27667;

XX DT 01-OCT-1998 (first entry)

XX DE Immunostimulatory oligodeoxyribonucleotide of the invention.

XX KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
 KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
 KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
 KW desensitisation therapy; artificial adjuvant; antibody generation; ss.

XX OS Synthetic.

XX PN WO9818810-A1.

XX PD 07-MAY-1998.

XX PF 30-OCT-1997; 97WO-US019791.

XX PR 30-OCT-1996; 96US-00738652.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PI Krieg AM, Kline JN;

XX PS WPI; 1998-272127/24.

XX PT New immunostimulatory nucleic acid molecules - which contain at least one
 PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
 PT or autoimmune disease.

XX PS Claim 35; Page 84; 109pp; English.

XX CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
 CC of the invention. The ODNs contain at least one unmethylated CpG
 CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
 CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
 CC thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26
 CC bases with the provision that N1 and N2 does not contain a CCG tetramer
 CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
 CC one nucleotide separates consecutive CpGs, X1 and X2 are selected from
 CC GpT, GpC, GpA, Apt and Apa, X3 and X4 are selected from Tpt or Cpt, N is
 CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
 CC does not contain a CCG tetramer or more than one CCG or CCG trimer. The
 CC ODNs activate lymphocytes in a subject and redirect a subject's immune
 CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other
 CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
 CC The ODNs can be used to treat or prevent an asthmatic disorder,
 CC autoimmune diseases, in desensitisation therapy, as an artificial
 CC adjuvant during antibody generation in a mammal such as a mouse or a
 CC human

XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
 |||||
 Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
AAZ41949
ID AAZ41949 standard; DNA; 20 BP.
AC AAZ41949;
XX
DT 24-JAN-2000 (first entry)
XX
DE IL-12 secretion inducing CpG oligonucleotide 94.
XX
KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW antigen presenting cell; infection; allergic disease.
XX
OS Synthetic.
XX
PN WO9951259-A2.
XX
PN PN
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US007335.
XX
PR 03-APR-1998; 98US-0080729P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Weiner G;
XX
DR WPI; 1999-620169/53.
XX
PT Novel synergistic combinations of immunostimulatory oligonucleotides and
PT immunopotentiating cytokines are useful for stimulating the immune
XX system.
XX
XX Example 8; Page 89; 91pp; English.
XX
CC Sequences AAZ41856-Z41949 are phosphorothioate CpG oligonucleotides which
CC are used in the invention to induce interleukin-12 (IL-12) secretion from
CC a human PBMC. The invention comprises stimulating an immune response in a
CC subject comprising administering to a subject exposed to an antigen, an
CC immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide
CC to induce a synergistic antigen specific immune response. The methods are
CC useful for treating cancer by stimulating an antigen specific immune
CC response against a cancer antigen. The methods can also be used to treat
CC neoplastic disorders in humans, including but not limited to: sarcoma,
CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
CC and glioma. The methods are also useful for treating infectious diseases
CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
CC The methods may also be used to treat allergic diseases, e.g. asthma. The
CC methods and compositions may also be applied to treat cancer and tumours
CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
CC agricultural livestock may also be treated and include leukaemia,
CC haemangioepithelioma and bovine ocular neoplasia. Chronic, infectious,
CC contagious diseases of sheep and goats caused by the bacterium
CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
CC caused by Jaagsiekte may also be treated. CpG oligonucleotides can be
CC useful in activating B cells, NK cells, and antigen presenting cells,
CC such as monocytes and macrophages. CpG oligonucleotides enhance antibody
CC dependent cellular cytotoxicity and can be used as an adjuvant in
CC conjunction with tumour antigens to protect against a tumour challenge
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
    |||||
Db 1 TCCATGACGTTCTCTGACGTT 20
    |||||

```

```

RESULT 6
AAZ78802
ID AAZ78802 standard; DNA; 20 BP.
XX
AC AAZ78802;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein CpG oligonucleotide 1.
XX
KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; primer; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO9933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1999; 98WO-BP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans MLJ, Gerard CMG;
XX
WPI; 1999-405485/34.
XX
Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
induce immune response to HPV.
XX
Claim 11; Page 36; 62pp; English.
XX
AAZ78791-X78801 represent nucleic acid sequences which encode novel
constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
HPV (represented in AAZ25375-Y25386). These constructs are optionally
linked to an immunological fusion partner and an immunomodulatory CpG
oligonucleotide. The products of the invention can be used to induce an
immune response in a patient to an HPV antigen. They can also be used for
preventing or treating HPV induced tumours. This sequence represents a
CpG oligonucleotide which is used in the method of the invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
Db 1 TCCATGACGTTCTGACGTT 20
RESULT 7
AAZ31943
ID AAZ31943 standard; DNA; 20 BP.
XX
AC AAZ31943;
XX
DT 26-JAN-2000 (first entry)
XX
DE CpG adjuvant oligo 1001.
XX
KW CpG adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
KW antigen; infection; allergy; cancer; therapy; ss.
XX
OS Synthetic.
XX

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PN WO9952549-A1.
XX
PD 21-OCT-1999.
XX
PF 29-MAR-1999; 99WO-EP002278.
XX
PR 09-APR-1998; 98GB-00007805.
PR 25-SEP-1998; 98GB-00020956.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Friede M, Hermand P;
XX
WPI; 1999-620290/53.
XX
Vaccine to protect against infections, allergy and cancer.
XX
Claim 16; Page 32; 52pp; English.
XX
This sequence represents a CpG adjuvant that can be used in the vaccine
composition of the invention. The vaccine comprises a polyoxyethylene
ether or ester (I), not in the form of a vesicle, pharmaceutically
acceptable excipient and an antigen (Ag) or antigenic composition. The
vaccine can be used to treat or prevent infections (by bacteria, viruses
or other parasites), allergy and cancer. (I), which are safe, easy to
sterilize and simple to administer, are powerful vaccine adjuvants, able
to induce a systemic immune response when administered (non-invasively)
to the mucosa. The response is at least as good as that from conventional
systemic injection. (I) are effective at low concentration, have low
reactogenicity and are well tolerated
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
Db 1 TCCATGACGTTCTGACGTT 20
RESULT 8
AAZ74237
ID AAV74237 standard; DNA; 20 BP.
XX
AC AAV74237;
XX
DT 20-MAR-2003 (revised)
DT 15-MAR-1999 (first entry)
XX
DE CpG-N motif S-ODN 1826 DNA.
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon; ss.
KW hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010408.
XX
PR 20-MAY-1997; 97US-0047209P.
PR 20-MAY-1997; 97US-0047233P.
XX
(OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (IOWA ) UNIV IOWA RES FOUND.
PA (QIAG-) QIAGEN GMBH.
XX

```


CC removing neutralising CpG (CpG-N) motifs and optionally inserting
 CC stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
 CC nucleic acid construct having enhanced immunostimulatory efficacy. The
 CC method can be used for immunisation against viral antigens, e.g. from
 CC hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
 CC parasite. They can also be used for expression of a therapeutic
 CC polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
 CC apoptotic proteins, interferons, hormones, clotting factors, ligands and
 CC receptors. (Updated on 20-MAR-2003 to correct PA field.)
 XX

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
 |||||
 DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
 AAX88536
 ID AAX88536 standard; DNA; 20 BP.

XX AAX88536;

DT 10-SEP-1999 (first entry)

XX Cytosine-guanosine dinucleotide motif oligonucleotide #3.

XX Cytosine-guanosine dinucleotide motif; CpG; immunomodulation;
 KW unmethylated; vaccine; immunostimulation; immune response;
 KW T-independent type 1 antigen; T-independent type 2 antigen;
 KW polysaccharide conjugate antigen; ss.

XX Synthetic.

XX WO9933488-A2.

XX 08-JUL-1999.

XX 18-DEC-1998; 98WO-EP008562.

XX 24-DEC-1997; 97GB-00027262.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Dalemans WLJ, Laferriere CAJ, Prieels J;

XX WPI; 1999-405369/34.

XX A vaccine composition for inducing a immune response to T-independent
 PT type 1 or type 2 antigen or polysaccharide conjugate antigen.

XX Claim 6; Page 31; 35pp; English.

CC The present invention describes a formulation (A) comprising a cytosine-
 CC guanosine dinucleotide motif (CpG) oligonucleotide and T-independent type
 CC 1 or type 2 antigens or polysaccharide conjugate antigen. The present
 CC sequence represent a specifically claimed CpG oligonucleotide. A vaccine
 CC composition comprising the formulation is used for inducing a immune
 CC response to T-independent type 1 or type 2 antigen or polysaccharide
 CC conjugate antigen. The use of immunostimulatory CpG oligonucleotide acts
 CC as an adjuvant to pneumococcal polysaccharides

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

DB 1 TCCATGACGTTCTCTGACGTT 20
 |||||

RESULT 12

AAZ28191

ID AAZ28191 standard; DNA; 20 BP.

XX AAZ28191;

XX 20-DEC-1999 (first entry)

XX Chlamydia trachomatis outer membrane protein gene-derived CpG oligo 4.

XX Heart disease; inflammatory; autoimmune; cardiomyopathy; adjuvant;

KW CpG motif; vaccine; ds.

XX Synthetic.

XX Chlamydia trachomatis.

PH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER = phosphorothioate linkage"

XX US5962636-A.

XX 05-OCT-1999.

XX 12-AUG-1998; 98US-00133774.

XX 12-AUG-1998; 98US-00133774.

XX (AMGE-) AMGEN CANADA INC.

XX Bachmaier K, Hessel AJ, Penninger JM, Neu N;

XX WPI; 1999-589735/50.

XX Peptides that induce or suppress inflammatory cardiomyopathy.

XX Example 2; Col 25; 17pp; English.

XX This sequence represents DNA encoding Chlamydia trachomatis 60 kD outer
 CC membrane protein (OMP) gene-derived CpG oligonucleotide 4. This
 CC oligonucleotide contains a CpG motif. It was tested for its ability to
 CC act as an adjuvant for the M7A-alpha peptide (AAZ42723), which can induce
 CC inflammatory cardiomyopathy (ICM) in mice. It was found to act as a
 CC potent immunostimulator, whereas a oligonucleotide from the same source
 CC which did not contain a CpG motif (AAZ28193) was hardly effective as an
 CC adjuvant. Inflammatory cardiomyopathy peptides (AAZ42723, AAZ42725-
 CC Y42731) can be used with such an adjuvant and an excipient in a vaccine
 CC for decreasing ICM

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13

AAZ61012

ID AAZ61012 standard; DNA; 20 BP.

XX AAZ61012;

XX 30-MAY-2000 (first entry)

XX Nucleotide sequence of an immunostimulatory CpG oligonucleotide.
DE
XX Immunostimulatory; stereoisomer; CpG oligonucleotide; Th2; Th1; asthma;
KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;
KW inflammatory disease; inflammatory bowel disease; autoimmune disease;
KW gingivitis; psoriasis; sepsis; ss.
XX
OS Synthetic.
XX WO200006588-A1.
XX 10-FEB-2000.
XX 27-JUL-1999; 99WO-US017100.
XX 27-JUL-1998; 98US-0094370P.
XX (IOWA) UNIV IOWA RES FOUND.
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX Krieg AM;
XX WPI; 2000-195254/17.
XX Immunostimulatory and immunoinhibitory stereoisomers of CpG
PT oligonucleotides useful for immunotherapy of cancer.
XX Disclosure; Page 12; 88pp; English.
XX AA260933-261015 represent immunostimulatory stereoisomers of CpG
CC oligonucleotides. The sequences are derived from generic nucleic acid
CC sequence, from which immunoinhibitory sequences may also be derived. The
CC immunostimulatory nucleic acids can be co-administered with an antigen to
CC induce an antigen-specific immune response. The immunostimulatory nucleic
CC acids can also be used in methods for redirecting a subject's immune
CC response from a Th2 to a Th1, for treating asthma, for desensitising a
CC subject against the occurrence of an allergic reaction in response to
CC contact with an allergen, for activating an immune cell, especially a
CC lymphocyte or a dendritic cell expressing a cancer antigen or for
CC treating cancer. The immunoinhibitory nucleic acid can be used to prevent
CC an immune response, especially where the immune response in the subject
CC is excessive due to having received an immune stimulating compound. The
CC immunoinhibitory nucleic acid can be used to treat a subject having or at
CC risk of an inflammatory disease, especially inflammatory bowel disease,
CC autoimmune disease, gingivitis, psoriasis and sepsis
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCCCTGACGTT 20
DB 1 TCCATGACGTTCCCTGACGTT 20
XX
RESULT 14
AAZ61010
ID AAZ61010 standard; DNA; 20 BP.
XX AAZ61010;
XX 30-MAY-2000 (first entry)
XX Nucleotide sequence of an immunostimulatory CpG oligonucleotide.
DE Immunostimulatory; stereoisomer; CpG oligonucleotide; Th2; Th1; asthma;
KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;
KW inflammatory disease; inflammatory bowel disease; autoimmune disease;
KW gingivitis; psoriasis; sepsis; ss.
XX

OS Synthetic.
XX WO200006588-A1.
XX 10-FEB-2000.
XX 27-JUL-1999; 99WO-US017100.
XX 27-JUL-1998; 98US-0094370P.
XX (IOWA) UNIV IOWA RES FOUND.
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX Krieg AM;
XX WPI; 2000-195254/17.
XX Immunostimulatory and immunoinhibitory stereoisomers of CpG
PT oligonucleotides useful for immunotherapy of cancer.
XX Disclosure; Page 12; 88pp; English.
XX AA260933-261015 represent immunostimulatory stereoisomers of CpG
CC oligonucleotides. The sequences are derived from generic nucleic acid
CC sequence, from which immunoinhibitory sequences may also be derived. The
CC immunostimulatory nucleic acids can be co-administered with an antigen to
CC induce an antigen-specific immune response. The immunostimulatory nucleic
CC acids can also be used in methods for redirecting a subject's immune
CC response from a Th2 to a Th1, for treating asthma, for desensitising a
CC subject against the occurrence of an allergic reaction in response to
CC contact with an allergen, for activating an immune cell, especially a
CC lymphocyte or a dendritic cell expressing a cancer antigen or for
CC treating cancer. The immunoinhibitory nucleic acid can be used to prevent
CC an immune response, especially where the immune response in the subject
CC is excessive due to having received an immune stimulating compound. The
CC immunoinhibitory nucleic acid can be used to treat a subject having or at
CC risk of an inflammatory disease, especially inflammatory bowel disease,
CC autoimmune disease, gingivitis, psoriasis and sepsis
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCCCTGACGTT 20
DB 1 TCCATGACGTTCCCTGACGTT 20
XX
RESULT 15
AAZ48025
ID AAZ48025 standard; DNA; 20 BP.
XX AAZ48025;
XX 08-MAR-2000 (first entry)
XX Immune remodeling inducing CpG oligonucleotide SEQ ID NO:105.
XX Haematopoiesis; regulation; CpG oligonucleotide; phosphorothioate;
KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
KW immune response; allergic reaction; infectious disease; asthma;
KW thrombocytopenia; immunohaemolytic disorder; genetic disorder;
KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;
KW rheumatoid arthritis; ss.
XX Synthetic.
XX WO9958118-A2.
XX 18-NOV-1999.
XX

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PF 14-MAY-1999; 99WO-IB001285.
XX
PR 14-MAY-1998; 98US-0085516P.
PR 02-FEB-1999; 99US-00241653.
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
PI Wagner H, Lipford G;
XX
XX WPI; 2000-062261/05.
XX
XX Use of CpG containing oligonucleotides for, e.g. inducing an antigen-
XX specific immune response.
XX
XX Example 1; Page 67; 116pp; English.
XX
XX The present invention describes a method using CpG containing
XX oligonucleotides (ONs) for regulating immune system remodeling and for
XX regulating haematopoiesis. The method for inducing an antigen-specific
XX immune response comprises: (1) administering an ON having a sequence
XX including at least the formula (I); and (2) exposing the subject to an
XX antigen at least 3 days after the ON is administered to the subject to
XX produce an antigen-specific immune response: 5' X1CGX2 3' (I), where the
XX ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and
XX X2 = nucleotides. The method can be used for inducing an immune response
XX against an antigen such as cells, cell extracts, proteins,
XX polysaccharides, polysaccharide conjugates, lipids, glycolipids,
XX carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
XX allergens. It can be used in a subject at risk of developing cancer or an
XX allergic reaction. It can also be used for treating an infectious
XX disease, allergic diseases and asthma, as well as thrombocytopaenia which
XX is drug-induced, due to an autoimmune disorder such as idiopathic
XX thrombocytopenic purpura, or resulting from accidental or therapeutic
XX radiation exposure. It can also be used for treating anaemia such as
XX -induced anaemia, immunohaemolytic disorder, genetic disorders such as
XX haemoglobinopathy and inherited haemolytic anaemia, inadequate production
XX despite adequate iron stores, chronic disease such as kidney failure, and
XX chronic inflammatory disorder such as rheumatoid arthritis, or anaemia
XX resulting from accidental or therapeutic radiation exposure. AA247932 to
XX AA248029 represent phosphorothioate CpG oligonucleotides used in the
XX exemplification of the present invention
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 3; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCATGACGTTCTCTGACGTT 20
XX |||||
XX Db 1 TCCATGACGTTCTCTGACGTT 20
XX
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
660.095 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	498	10	CL978668
C 2	20	100.0	2799	10	CL978665
C 3	18.4	92.0	372	10	CW048863
C 4	18.4	92.0	460	10	CW036410
C 5	18.4	92.0	886	9	CC709713
C 6	17.4	87.0	698	7	CN928980
C 7	17.4	87.0	1062	10	CL970339
C 8	17	85.0	562	10	CW062877
C 9	17	85.0	659	10	CW124513
C 10	17	85.0	687	10	CW372789
C 11	17	85.0	703	10	CW631458
C 12	17	85.0	782	10	CW031589
C 13	17	85.0	1088	6	CD505499
C 14	17	85.0	2805	10	CL965273
C 15	16.8	84.0	287	2	BF713668
C 16	16.8	84.0	389	10	CG260054
C 17	16.8	84.0	464	1	AA171941
C 18	16.8	84.0	497	10	CL179555
C 19	16.8	84.0	510	10	CW218453
C 20	16.8	84.0	516	2	BF156008
C 21	16.8	84.0	546	1	AW065908
C 22	16.8	84.0	557	6	CA158051

C 23	16.8	84.0	614	6	CA113844
C 24	16.8	84.0	628	10	CW444501
C 25	16.8	84.0	646	6	CA109803
C 26	16.8	84.0	663	6	CA153904
C 27	16.8	84.0	668	6	CA264770
C 28	16.8	84.0	683	6	CA182313
C 29	16.8	84.0	715	5	BUZ53412
C 30	16.8	84.0	729	7	CV181077
C 31	16.8	84.0	758	9	CC110844
C 32	16.8	84.0	779	8	DR806582
C 33	16.8	84.0	794	10	CG334934
C 34	16.8	84.0	797	10	CNS02N06
C 35	16.8	84.0	814	5	BUZ05165
C 36	16.8	84.0	821	11	CNS03G84
C 37	16.8	84.0	842	10	CG319646
C 38	16.8	84.0	864	10	CG318330
C 39	16.8	84.0	908	6	CD791886
C 40	16.8	84.0	911	10	AG891719
C 41	16.8	84.0	915	10	CG318342
C 42	16.8	84.0	958	5	BQ882047
C 43	16.8	84.0	992	11	CNS040Q4
C 44	16.8	84.0	994	11	CNS042IL
C 45	16.8	84.0	1460	8	DN675999

ALIGNMENTS

RESULT 1
CL978668/c
LOCUS CL978668 498 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC032298 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL978668
VERSION CL978668.1 GI:52411839
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 498)
AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES

source
1..498
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 498;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTCCTGACGTT 20
|||||
DB 83 TCCATGACGTCCTGACGTT 64

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RESULT 2
CL978665/c
LOCUS
DEFINITION
Oryza sativa indica cultivar-group) genomic, GSS 21-SEP-2004
ACCESSION
CL978665
VERSION
CL978665.1 GI:52411833
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Zosterocaulales; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 2799)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..2799
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"
ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 2354 TCCATGACGTTCTGACGTT 2335
|||||

RESULT 3
CW048863/c
LOCUS
DEFINITION
Oryza sativa indica cultivar-group) genomic, GSS 21-SEP-2004
ACCESSION
CW048863
VERSION
CW048863.1 GI:52411833
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Zosterocaulales; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 2799)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..2799
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"
ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 2799;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 2354 TCCATGACGTTCTGACGTT 2335
|||||

RESULT 4
CW036410/c
LOCUS
DEFINITION
Sorghum bicolor genomic clone 10503742, genomic survey
sequence.
ACCESSION
CW036410
VERSION
CW036410.1 GI:54713140
KEYWORDS
GSS.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Zosterocaulales; Oryzaceae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 460)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McComb, W.R., Jeddeloh, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 460.
FEATURES
source
1..460
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"

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```

Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: m column: 17
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 372.
FEATURES
source
1..372
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="10513675"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCKS(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCKS(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."
ORIGIN
Query Match 92.0%; Score 18.4; DB 10; Length 372;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 267 TCCATGACGTTCCGACGTT 248
|||||

RESULT 4
CW036410/c
LOCUS
DEFINITION
Sorghum bicolor genomic clone 10503742, genomic survey
sequence.
ACCESSION
CW036410
VERSION
CW036410.1 GI:54713140
KEYWORDS
GSS.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Zosterocaulales; Oryzaceae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 460)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McComb, W.R., Jeddeloh, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 267 row: k column: 20
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 460.
FEATURES
source
1..460
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"

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/db_xref="taxon:4558"
/clone="10503742"
/clone_lib="Sorghum methylation filtered library (libid:
104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly_eneared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match          92.0%; Score 18.4; DB 10; Length 460;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGACGTT 20
|||||
Db 291 TCCATGAGCTTCGGACGTT 272

RESULT 5
CC709713          886 bp DNA linear GSS 19-JUN-2003
LOCUS OGUBY23TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0404D21,
genomic survey sequence.
ACCESSION CC709713
VERSION CC709713.1 GI:32114489
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 886)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Other GSSs: OGUBY23TH
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
FEATURES
Location/Qualifiers
source
1..886
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0404D21"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match          92.0%; Score 18.4; DB 9; Length 886;
Best Local Similarity 95.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGACGTT 20
|||||
Db 31 TCCATGAGCTTCGGACGTT 50

RESULT 6
CN928980
LOCUS
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DEFINITION 00601AEPAA006237HT (AEPa) pinkie expanding leaf Malus x domestica
CDNA clone AEPAA006237, mRNA sequence.
ACCESSION CN928980
VERSION CN928980.1 GI:48401793
KEYWORDS EST.
SOURCE Malus x domestica
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 698)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES
Location/Qualifiers
source
1..698
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AEPAA006237"
/tissue_type="Leaf"
/dev_stage="Expanding"
/clone_lib="(AEPa) Pinkie expanding leaf"
/notes="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN
Query Match          87.0%; Score 17.4; DB 7; Length 698;
Best Local Similarity 94.7%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCATGAGCTTCCTGACGTT 19
|||||
Db 86 TCAATGAGCTTCCTGACGTT 104

RESULT 7
CN970339/c
LOCUS CL970339
DEFINITION OsIFCC041133 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION CL970339
VERSION CL970339.1 GI:52395287
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 1062)
AUTHORS Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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FEATURES
  source      Location/Qualifiers
1..1062      /organism="Oryza sativa (indica cultivar-group)"
             /mol_type="genomic DNA"
             /db_xref="taxon:39946"
             /clone_lib="Oryza sativa Express Library"
             /note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 1062;
Best Local Similarity 94.7%; Pred. No. 9.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGT 19
    |||||
Db 599 TCCATGACGTTCTGCGGT 581
    |||||

RESULT 8
CW062877
LOCUS      562 bp DNA linear GSS 28-OCT-2004
DEFINITION 104_308_10521584_1_30092 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10521584, genomic survey
            sequence.
ACCESSION  CW062877
VERSION     CW062877.1 GI:54739607
KEYWORDS   Sorghum bicolor (sorghum)
SOURCE     Sorghum bicolor
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
            1 (bases 1 to 562)
REFERENCE  Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and
            Martienssen,R.A.
            Sorghum genome sequencing by methylation filtration
            PLOS Biol. 3 (1), e13 (2005)
            15660154
COMMENT    Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Seq primer: M13(40) Forward
            Plate: 308 row: 9 column: 06
            Class: methylation filtered
            High quality sequence stop: 562.
            Location/Qualifiers
            1..562
            /organism="Sorghum bicolor"
            /mol_type="genomic DNA"
            /cultivar="ATx623"
            /db_xref="taxon:4558"
            /clone="10521584"
            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."

ORIGIN
Query Match      85.0%; Score 17; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGAC 17
    |||||
Db 545 TCCATGACGTTCTGAC 529
    |||||

RESULT 10
CW372789
LOCUS      687 bp DNA linear GSS 01-NOV-2004
DEFINITION fbb001f048n16f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fbb001f048n16, genomic survey
            sequence.
ACCESSION  CW372789
VERSION     CW372789.1 GI:55091233
KEYWORDS   Sorghum bicolor (sorghum)
SOURCE     Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
            1 (bases 1 to 659)
REFERENCE  Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and
            Martienssen,R.A.
            Sorghum genome sequencing by methylation filtration
            PLOS Biol. 3 (1), e13 (2005)
            15660154
COMMENT    Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Seq primer: Sfwor Forward
            Plate: 504 row: 9 column: 11
            Class: methylation filtered
            High quality sequence stop: 659.
            Location/Qualifiers
            1..659
            /organism="Sorghum bicolor"
            /mol_type="genomic DNA"
            /cultivar="ATx623"
            /db_xref="taxon:4558"
            /clone="11111819"
            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."

ORIGIN
Query Match      85.0%; Score 17; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGAC 17
    |||||
Db 545 TCCATGACGTTCTGAC 529
    |||||

RESULT 10
CW372789
LOCUS      687 bp DNA linear GSS 01-NOV-2004
DEFINITION fbb001f048n16f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fbb001f048n16, genomic survey
            sequence.
ACCESSION  CW372789
VERSION     CW372789.1 GI:55091233
KEYWORDS   Sorghum bicolor (sorghum)
SOURCE     Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
            1 (bases 1 to 659)
REFERENCE  Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and
            Martienssen,R.A.
            Sorghum genome sequencing by methylation filtration
            PLOS Biol. 3 (1), e13 (2005)
            15660154
COMMENT    Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Seq primer: Sfwor Forward
            Plate: 504 row: 9 column: 11
            Class: methylation filtered
            High quality sequence stop: 659.
            Location/Qualifiers
            1..659
            /organism="Sorghum bicolor"
            /mol_type="genomic DNA"
            /cultivar="ATx623"
            /db_xref="taxon:4558"
            /clone="11111819"
            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."

ORIGIN
Query Match      85.0%; Score 17; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGAC 17
    |||||
Db 545 TCCATGACGTTCTGAC 529
    |||||

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ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 687)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and Martienssen,R.A.

TITLE Sorghum genome sequencing by methylation filtration
JOURNAL PLoS Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: f8bb001f048 row: n column: 16
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 687.

FEATURES
source Location/Qualifiers
1..687
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="f8bb001f048n16"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBGSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly-sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBGSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCGAC 17
|||||
Db 102 TCCATGACGTTCTCGAC 86

RESULT 11
CW631458/c
LOCUS CW631458
DEFINITION OP__Ba0057L22.f OP__Ba Oryza punctata genomic clone OP__Ba0057L22
5', Genomic survey sequence.
ACCESSION CW631458
VERSION CW631458.1 GI:54665420
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 703)
AUTHORS SanMiguel P., Westerman,R., Kim,H., Yu,Y., Wisotski,M., Yost,D., Stun,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
OMAP Project - Purdue University
Unpublished (2004)
TITLE Oryza punctata genome sequencing by methylation filtration
JOURNAL PLoS Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 260 row: e column: 06
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 782.

FEATURES
source Location/Qualifiers
1..782
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"

Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lcy version 1.198.
Bases 36-738 of the raw sequence (length 1024) were retained after clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0057 row: L column: 22
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES
source Location/Qualifiers
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/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP__Ba0057L22"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP__Ba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCGAC 17
|||||
Db 259 TCCATGACGTTCTCGAC 243

RESULT 12
CW031589
LOCUS CW031589
DEFINITION CW031589 782 bp DNA linear GSS 28-OCT-2004
104 260_10500896 114 30365 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 10500896, genomic survey sequence.
ACCESSION CW031589
VERSION CW031589.1 GI:54708321
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 782)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and Martienssen,R.A.

TITLE Sorghum genome sequencing by methylation filtration
JOURNAL PLoS Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 260 row: e column: 06
Seq primer: M13/pUC Forward
Class: methylation filtered
High quality sequence stop: 782.

FEATURES
source Location/Qualifiers
1..782
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"

/clone="10500896"
 /clone_lib="Sorghum methylation filtered library (LibID: 104)"
 /note="Organ: leaf; Vector: pBSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 782;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGAC 17
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 Db 330 TCCATGACGTTCTCTGAC 346

RESULT 13

LOCUS CD505499 1088 bp mRNA linear EST 12-JUN-2003
 DEFINITION CDA74-A09.xld-t SHGC-CDA Gasterosteus aculeatus cDNA clone
 CDA74-A09 5', mRNA sequence.

ACCESSION CD505499
 VERSION CD505499.1 GI:31436068
 KEYWORDS EST.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.

REFERENCE

AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from Gasterosteus aculeatus
 JOURNAL Unpublished (2003)

COMMENT

HHMI and Department of Developmental Biology
 Stanford University School of Medicine
 Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
 Tel: 650 725 5954
 Fax: 650 725 7739
 Email: kingsley@cngm.stanford.edu
 Plate: 74

High quality sequence stop: 772.

FEATURES

Source

1..1088
 Location/Qualifiers
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Salinas river, CA"
 /db_xref="taxon:69293"
 /clone="CDA74-A09"
 /sex="mixed male and female"
 /tissue_type="heads and internal organs combined"
 /dev_stage="adult"
 /clone_lib="SHGC-CDA"

/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI (5' adaptor); Site 2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."

ORIGIN

Query Match 85.0%; Score 17; DB 6; Length 1088;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGAC 17
 |||||
 Db 308 TCCATGACGTTCTCTGAC 324

RESULT 14

LOCUS CL965273 2805 bp DNA linear GSS 21-SEP-2004
 DEFINITION OsIFCC012064 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL965273
 VERSION CL965273.1 GI:52385237
 KEYWORDS GSS.

SOURCE

ORGAISM Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
 TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

JOURNAL

Unpublished (2004)

COMMENT

Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

FEATURES

Source

1..2805
 Location/Qualifiers
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_lib="Oryza sativa Express Library"
 /note="Oryza sativa exon trapped genomic sequences "

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 2805;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGAC 17
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 Db 2372 TCCATGACGTTCTCTGAC 2356

RESULT 15

LOCUS BF713668 287 bp mRNA linear EST 31-DEC-2001
 DEFINITION ESTPBL223 differential display RT-PCR clones Sus scrofa cDNA clone BL223, mRNA sequence.

ACCESSION BF713668
 VERSION BF713668.1 GI:18002858
 KEYWORDS EST.

SOURCE

ORGAISM Sus scrofa (pig)

Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE

AUTHORS Ponsuksilli,S., Wimmers,K. and Schellander,K.

TITLE Identification of porcine liver ESTs by differential display RT-PCR
JOURNAL Unpublished (2001)
COMMENT Contact: Ponsuksili S
Institute of Animal Breeding Science
University of Bonn
Endenicher Allee 15, Bonn 53115, Germany
Seq primer: 17 SP6
High quality sequence stop: 287
POLYA=No.

FEATURES Location/Qualifiers
source 1..287
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="BL223"
/clone_lib="differential display RT-PCR clones"
/note="Organ: liver; cDNA fragments obtained from
differential display RT-PCR banding patterns were cloned
into pGEM"

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 287;
Best Local Similarity 90.0%; Pred No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 14 TCCATGACGTTCTCTGATGCT 33

Search completed: May 4, 2006, 07:17:44
Job time : 1421.59 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 07:24:16 ; Search time 298.851 Seconds
(without alignments)
553.412 Million cell updates/sec

Title: US-10-789-758A-6

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-760-506-3
2	20	100.0	20	3	US-09-768-012-3
3	20	100.0	20	3	US-09-824-468-100
4	20	100.0	20	3	US-09-824-468-105
5	20	100.0	20	3	US-09-949-194-1
6	20	100.0	20	3	US-09-917-222-1
7	20	100.0	20	3	US-09-800-266A-86
8	20	100.0	20	3	US-09-800-266A-90
9	20	100.0	20	3	US-09-895-007A-86
10	20	100.0	20	3	US-09-895-007A-90
11	20	100.0	20	3	US-09-920-313-86
12	20	100.0	20	3	US-09-920-313-90
13	20	100.0	20	3	US-09-888-326-560
14	20	100.0	20	3	US-09-888-326-561
15	20	100.0	20	3	US-09-888-326-562
16	20	100.0	20	3	US-09-888-326-563
17	20	100.0	20	3	US-09-818-918-10
18	20	100.0	20	3	US-09-931-583-47
19	20	100.0	20	3	US-09-776-479-69
20	20	100.0	20	3	US-09-776-479-137
21	20	100.0	20	3	US-09-776-479-152
22	20	100.0	20	3	US-09-776-479-153
23	20	100.0	20	3	US-09-776-479-223

24	20	100.0	20	3	US-09-776-479-302	Sequence 302, App
25	20	100.0	20	3	US-09-776-479-948	Sequence 948, App
26	20	100.0	20	3	US-09-776-479-949	Sequence 949, App
27	20	100.0	20	3	US-09-776-479-950	Sequence 950, App
28	20	100.0	20	3	US-09-776-479-951	Sequence 951, App
29	20	100.0	20	3	US-09-776-479-952	Sequence 952, App
30	20	100.0	20	3	US-09-776-479-953	Sequence 953, App
31	20	100.0	20	3	US-09-776-479-954	Sequence 954, App
32	20	100.0	20	3	US-09-776-479-955	Sequence 955, App
33	20	100.0	20	3	US-09-776-479-956	Sequence 956, App
34	20	100.0	20	3	US-09-776-479-957	Sequence 957, App
35	20	100.0	20	3	US-09-776-479-958	Sequence 958, App
36	20	100.0	20	3	US-09-776-479-1023	Sequence 1023, App
37	20	100.0	20	3	US-09-954-987B-83	Sequence 83, Appli
38	20	100.0	20	3	US-09-967-464-1	Sequence 1, Appli
39	20	100.0	20	3	US-09-984-365-42	Sequence 42, Appli
40	20	100.0	20	3	US-09-984-365-42	Sequence 69, Appli
41	20	100.0	20	3	US-09-776-479-137	Sequence 137, App
42	20	100.0	20	3	US-09-776-479-152	Sequence 152, App
43	20	100.0	20	3	US-09-776-479-153	Sequence 153, App
44	20	100.0	20	3	US-09-776-479-223	Sequence 223, App
45	20	100.0	20	3	US-09-776-479-302	Sequence 302, App

ALIGNMENTS

RESULT 1
US-09-760-506-3
; Sequence 3, Application US/09760506
; Publication No. US20010034330A1
; GENERAL INFORMATION:
; APPLICANT: Kensil, Charlotte
; TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of Cpg and Saponin and Methods Thereof
; FILE REFERENCE: 8449-153-999
; CURRENT APPLICATION NUMBER: US/09/760,506
; CURRENT FILING DATE: 2002-01-12
; PRIOR APPLICATION NUMBER: 60/200,853
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/175,840
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/128,608
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/095,913
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-09-760-506-3

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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTGACGTT 20
Db 1 TCCATGACGTTCTGACGTT 20

RESULT 2
US-09-768-012-3
; Sequence 3, Application US/09768012
; Patent No. US2001004416A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: McCluskie, Michael J.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for

```
; TITLE OF INVENTION: Inducing a Th2 Immune Response
; FILE REFERENCE: C1040/7010/HCL/MAT
; CURRENT APPLICATION NUMBER: US/09/769,012
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,461
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; NAME/KEY: modified_base
; LOCATION: (8)...(8)
; OTHER INFORMATION: Cytosine is unmethylated.
; NAME/KEY: modified_base
; LOCATION: (17)...(17)
; OTHER INFORMATION: Cytosine is unmethylated.
US-09-768-012-3
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TCCATGACGTTCTCTGACGTT 20
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RESULT 3
US-09-824-468-100
; Sequence 100, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-100
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TCCATGACGTTCTCTGACGTT 20
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RESULT 4
US-09-824-468-105
; Sequence 105, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
```

```
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-105
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
US-09-949-194-1
; Sequence 1, Application US/09949194
; Patent No. US20020091097A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
; FILE REFERENCE: C1037/7021 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/949,194
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230,637
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-949-194-1
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TCCATGACGTTCTCTGACGTT 20
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RESULT 6
US-09-917-222-1
; Sequence 1, Application US/09917222
; Patent No. US20020110569A1
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: VACCINES FOR BROAD SPECTRUM PROTECTION
; TITLE OF INVENTION: AGAINST DISEASES CAUSED BY NEISSERIA MENINGITIDIS
; FILE REFERENCE: CHOR001
; CURRENT APPLICATION NUMBER: US/09/917,222
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,495
; PRIOR FILING DATE: 2000-07-27
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG nucleotides
US-09-917-222-1

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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 7
US-09-800-266A-86
; Sequence 86, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: C1037/7017(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,214
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-86

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 8
US-09-800-266A-90
; Sequence 90, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: C1037/7017(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,214
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-90

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 9
US-09-895-007A-86
; Sequence 86, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,368
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-86

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 10
US-09-895-007A-90
; Sequence 90, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,368
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-90
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Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
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Db 1 TCCATGACGTTCTGACGTT 20

RESULT 11

US-09-920-313-86
; Sequence 86, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-86

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTGACGTT 20

RESULT 12

US-09-920-313-90
; Sequence 90, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-90

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTGACGTT 20

RESULT 13

US-09-888-326-560
; Sequence 560, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-560

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTGACGTT 20

RESULT 14

US-09-888-326-561
; Sequence 561, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 561
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-888-326-561

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTGACGTT 20

RESULT 15

US-09-888-326-562

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; Sequence 562, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 562
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-562
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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 TCCATGACGTTCCCTGACGTT 20
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Db 1 TCCATGACGTTCCCTGACGTT 20
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Search completed: May 4, 2006, 09:01:07
Job time : 299.851 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 08:17:52 ; Search time 456.437 Seconds
(without alignments)
178.449 Million cell updates/sec

Title: US-10-789-758A-6
Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA-New*

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- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq*
- 4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq*
- 5: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 7: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq1*
- 8: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1*
- 11: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2*
- 12: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3*
- 13: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq4*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq*
- 15: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2*
- 16: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3*
- 17: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4*
- 18: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq5*
- 19: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-10-469-561-5
2	20	100.0	20	10	US-10-619-279-10
3	20	100.0	20	10	US-10-435-656-10
4	20	100.0	20	10	US-10-881-661-3
5	20	100.0	20	11	US-10-533-634-43
6	20	100.0	20	12	US-10-382-822-10
7	20	100.0	20	14	US-11-296-572-10
8	20	100.0	20	17	US-11-025-858-3
9	20	100.0	20	17	US-11-025-858-7
10	20	100.0	20	17	US-11-127-654-63
11	20	100.0	20	17	US-11-127-654-82
12	20	100.0	20	17	US-11-127-654-130
13	20	100.0	20	17	US-11-127-654-145
14	20	100.0	20	17	US-11-127-654-146

15	20	100.0	20	17	US-11-127-654-292	Sequence 292, Appl
16	20	100.0	20	17	US-11-127-654-916	Sequence 916, Appl
17	20	100.0	20	17	US-11-154-324-1	Sequence 1, Appl
18	20	100.0	20	17	US-11-089-426-22	Sequence 22, Appl
19	20	100.0	20	17	US-11-134-918-10	Sequence 10, Appl
20	20	100.0	20	17	US-11-031-460-10	Sequence 10, Appl
21	20	100.0	20	17	US-11-087-177-45	Sequence 45, Appl
22	20	100.0	20	17	US-11-114-325-1	Sequence 1, Appl
23	20	100.0	20	17	US-11-033-039-906	Sequence 906, Appl
24	20	100.0	20	17	US-11-067-587-10	Sequence 10, Appl
25	20	100.0	20	17	US-11-141-690-3	Sequence 3, Appl
26	20	100.0	20	17	US-11-178-316-19	Sequence 19, Appl
27	20	100.0	20	17	US-11-099-683-61	Sequence 61, Appl
28	20	100.0	20	18	US-11-081-882-1	Sequence 1, Appl
29	20	100.0	20	18	US-11-268-170-16	Sequence 16, Appl
30	20	100.0	20	18	US-10-482-112D-2	Sequence 2, Appl
31	18.4	92.0	20	17	US-11-127-654-221	Sequence 221, Appl
32	18.4	92.0	1191	10	US-10-750-185-47485	Sequence 47485, A
33	18.4	92.0	1191	10	US-10-750-623-47485	Sequence 47485, A
34	18	90.0	20	10	US-10-497-591A-37	Sequence 37, Appl
35	18	90.0	20	10	US-10-497-591A-38	Sequence 38, Appl
36	18	90.0	20	17	US-11-127-654-303	Sequence 303, Appl
37	17	85.0	17	10	US-10-619-279-70	Sequence 70, Appl
38	17	85.0	17	12	US-10-382-822-70	Sequence 70, Appl
39	17	85.0	17	17	US-11-127-654-66	Sequence 66, Appl
40	16.8	84.0	20	10	US-10-497-591A-12	Sequence 12, Appl
41	16.8	84.0	20	10	US-10-469-561-9	Sequence 9, Appl
42	16.8	84.0	20	10	US-10-619-279-7	Sequence 7, Appl
43	16.8	84.0	20	10	US-10-619-279-73	Sequence 73, Appl
44	16.8	84.0	20	10	US-10-435-656-7	Sequence 7, Appl
45	16.8	84.0	20	10	US-10-435-656-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-10-469-561-5
; Sequence 5, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-5

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCCCTGACGTT 20

Db 1 TCCATGACGTTCCCTGACGTT 20

RESULT 2
US-10-619-279-10
; Sequence 10, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-10

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 1 TCCATGACGTTCTGACGTT 20

RESULT 3
US-10-435-656-10
; Sequence 10, Application US/10435656
; Publication No. US2005027604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-10

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 1 TCCATGACGTTCTGACGTT 20

RESULT 4
US-10-881-661-3
; Sequence 3, Application US/10881661

; Publication No. US20060002928A1
; GENERAL INFORMATION:
; APPLICANT: Radhakrishnan, Suresh
; APPLICANT: Pease, Larry R.
; APPLICANT: Iijima, Koji
; APPLICANT: Kita, Hirohito
; TITLE OF INVENTION: Methods And Molecules For Modulating An Immune Response
; FILE REFERENCE: 07039-520001
; CURRENT APPLICATION NUMBER: US/10/881,661
; CURRENT FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-881-661-3

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 1 TCCATGACGTTCTGACGTT 20

RESULT 5
US-10-533-634-43
; Sequence 43, Application US/10533634
; Publication No. US20060019239A1
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Ivins, Bruce
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF PREVENTING INFECTIONS FROM BIOTERRORISM AGENTS WITH
; FILE REFERENCE: 4239-67021-06
; CURRENT APPLICATION NUMBER: US/10/533,634
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034523
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,964
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: K oligonucleotide
US-10-533-634-43

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 TCCATGACGTTCTGACGTT 20
|||||
DB 1 TCCATGACGTTCTGACGTT 20

RESULT 6
US-10-382-822-10
; Sequence 10, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.

Qy 1 TCCATGACGTTCTTGACGTT 20

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Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TCCATGACGTTCTCTGACGTT 20
|||||

pb 1 TCCATGACGTTCTCTGACGTT 20
|||||

RESULT 10
US-11-127-654-63
; Sequence 63, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-63

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
US-11-127-654-82
; Sequence 82, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: m5C
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: m5C
US-11-127-654-82

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-11-127-654-130
; Sequence 130, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-130

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; Sequence 145, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-145

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
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; SOFTWARE: PatentIn version 3.2
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; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-146

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Matches 20; Conservative 0;

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; Sequence 292, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
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; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-292

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Db 1 TCCATGACGTTCTGACGTT 20

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Garcon,N. and Voss,G.
TITLE Vaccine
JOURNAL Patent: WO 0100232-A 7 04-JAN-2001;
SmithKline Beecham Biologics SA (BE)
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LOCUS Synthetic nucleotide with (GACGTC) structure, having immunomodulation
DEFINITION activities.
ACCESSION E04644
VERSION E04644.1 GI:2172840
KEYWORDS JP 1992352724-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 45)
AUTHORS Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O.,
Makino,T. and Shimada,S.
TITLE IMMUNOMODULATION TYPE THERAPEUTIC AGENT
JOURNAL Patent: JP 1992352724-A 1 07-DEC-1992;
MITSUI TOATSU CHEM INC
COMMENT
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992352724-A/65
PD 07-DEC-1992
PF 18-JUL-1991 JP 1991178058
PR 27-JUL-1990 JP 90P 197778
PI TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO
ETSURO,
PI YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
PC A61K31/70,A61K31/70,A61K31/70//C07H21/04;
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FH Key Location/Qualifiers
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FT /note="synthetic nucleotide prepared as control".
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RESULT 5
AX105264
LOCUS Sequence 163 from Patent WO0122990.
DEFINITION
ACCESSION AX105264
VERSION AX105264.1 GI:13921414
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Hartmann,G.D., Bratzler,R.L. and Krieg,A.U.
TITLE Methods related to immunostimulatory nucleic acid-induced interferon
JOURNAL Patent: WO 0122990-A 163 05-APR-2001;
Coley Pharmaceutical Group, Inc. (US) ; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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/note="Synthetic Oligonucleotide"

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RESULT 6

LOCUS A36735 268 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent EP0584023.
ACCESSION A36735
VERSION A36735.1 GI:2294002
KEYWORDS
SOURCE Mycobacterium bovis
ORGANISM Mycobacterium bovis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE Mabilat,C. and Pechere,J.
AUTHORS Mycobacteria DNA fragments, amplification primers, hybridization
TITLE probes, reagents and detection process of mycobacteria
JOURNAL Patent: EP 0584023-A 1 23-FEB-1994;
BIO MERIEUX (FR)
COMMENT Other publication CA 2103933 940213
Other publication FR 2694754 940218.
FEATURES
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Db 29 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 63

RESULT 7

LOCUS A36736 268 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 2 from Patent EP0584023.
ACCESSION A36736
VERSION A36736.1 GI:2294003
KEYWORDS
SOURCE Mycobacterium microti
ORGANISM Mycobacterium microti
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE Mabilat,C. and Pechere,J.
AUTHORS Mycobacteria DNA fragments, amplification primers, hybridization
TITLE probes, reagents and detection process of mycobacteria
JOURNAL Patent: EP 0584023-A 2 23-FEB-1994;
BIO MERIEUX (FR)
COMMENT Other publication CA 2103933 940213
Other publication FR 2694754 940218.
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Db 29 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 63

RESULT 8

LOCUS AR066278 268 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5849901.
ACCESSION AR066278
VERSION AR066278.1 GI:5996494
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization
probes, reagents and method for the detection of mycobacteria
JOURNAL Patent: US 5849901-A 1 15-DEC-1998;
FEATURES Location/Qualifiers
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Db 29 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 63

RESULT 9

LOCUS AR066279 268 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5849901.
ACCESSION AR066279
VERSION AR066279.1 GI:5996495
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization
probes, reagents and method for the detection of mycobacteria
JOURNAL Patent: US 5849901-A 2 15-DEC-1998;
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Best Local Similarity 94.3%; Pred. No. 4.3;
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Db 29 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 63

RESULT 10

133087

LOCUS I33087 268 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5589585.
ACCESSION I33087
VERSION I33087.1 GI:1823878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 1 31-DEC-1996;
FEATURES Location/Qualifiers
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Best Local Similarity 94.3%; Pred. No. 4.3;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
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29 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 63

LOCUS I33088 268 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5589585.
ACCESSION I33088
VERSION I33088.1 GI:1823879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 2 31-DEC-1996;
FEATURES Location/Qualifiers
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QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
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LOCUS I33089 314 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 23 from patent US 5589585.
ACCESSION I33109
VERSION I33109.1 GI:1823900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 314)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 23 31-DEC-1996;
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52 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 86

LOCUS A30752 342 bp DNA linear PAT 24-JUL-1996
DEFINITION Mycobacterial sp. DNA for 65 kDa-like mycobacterial antigen (partial).
ACCESSION A30752
VERSION A30752.1 GI:1567052
KEYWORDS
SOURCE Mycobacterium
ORGANISM Mycobacterium
REFERENCE 1 (bases 1 to 342)
AUTHORS
TITLE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
JOURNAL NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
FEATURES Patent: WO 9012875-A 6 01-NOV-1990;
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DEFINITION Sequence 1 from patent US 5589585.
ACCESSION I33087
VERSION I33087.1 GI:1823878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 1 31-DEC-1996;
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29 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 63

LOCUS I33088 268 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5589585.
ACCESSION I33088
VERSION I33088.1 GI:1823879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 268)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 2 31-DEC-1996;
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29 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 63

LOCUS I33089 314 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 23 from patent US 5589585.
ACCESSION I33109
VERSION I33109.1 GI:1823900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 314)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments, probes and amplification primers of the 65 kd antigen of mycobacteria
JOURNAL Patent: US 5589585-A 23 31-DEC-1996;
FEATURES Location/Qualifiers
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LOCUS A30752 342 bp DNA linear PAT 24-JUL-1996
DEFINITION Mycobacterial sp. DNA for 65 kDa-like mycobacterial antigen (partial).
ACCESSION A30752
VERSION A30752.1 GI:1567052
KEYWORDS
SOURCE Mycobacterium
ORGANISM Mycobacterium
REFERENCE 1 (bases 1 to 342)
AUTHORS
TITLE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
JOURNAL NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
FEATURES Patent: WO 9012875-A 6 01-NOV-1990;
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LOCUS
DEFINITION Mycobacterial sp. DNA for 65 kDa-like mycobacterial antigen
          342 bp DNA linear PAT 24-JUL-1996
          (partial).
ACCESSION A30753
VERSION A30753.1 GI:1567053
KEYWORDS
SOURCE Mycobacterium
ORGANISM Mycobacterium
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 342)
AUTHORS
TITLE NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE
       SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF
       SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
JOURNAL Patent: WO 9012875-A 7 01-NOV-1990;
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GenCore version 5.1.7
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Title: US-10-789-758A-7

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5	31.8	58.9	268	2	AaQ57762 Mycobacte
6	31.8	58.9	268	2	AaQ57761 Mycobacte
7	31.8	58.9	342	2	AaQ06507 Encodes p
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41	31.8	58.9	110000	4	AAI99683_05
42	30.2	55.9	45	4	AAH46030
43	30.2	55.9	268	2	AAQ57763
44	30.2	55.9	604	9	ACF04300
45	30.2	55.9	604	9	ACF04279

ALIGNMENTS

RESULT 1

AAF27753

ID AAF27753 standard; DNA; 54 BP.

AC AAF27753;

DT 03-APR-2001 (first entry)

DE P. falciparum vaccine CpG oligonucleotide WD1007.

XX Plasmodium falciparum; malaria; CpG oligonucleotide; vaccine; sporozoite; ds.

OS Unidentified.

PN WO200100231-A2.

XX 04-JAN-2001.

PF 23-JUN-2000; 2000WO-EP005841.

PR 29-JUN-1999; 99GB-00015204.

XX (SMTK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Cohen J, Garcon N, Voss G;

DR WPI; 2001-112392/12.

PT New vaccine formulation, useful for preventing and treating plasmodium infection in a patient, comprises malaria antigen and immunostimulatory CpG oligonucleotide.

PS Claim 8; Page 16; 22pp; English.

CC The present invention describes a vaccine comprising a malaria antigen and an immunostimulatory CpG oligonucleotide. This is useful in the prevention and treatment of malaria caused by Plasmodium falciparum infection

XX Sequence 54 BP; 6 A; 15 C; 16 G; 17 T; 0 U; 0 Other;

SQ

XX	AAQ20698;
AC	11-MAY-1992 (first entry)
XX	Immunostimulatory oligonucleotide #1 contg. palindrome.
DT	natural killer cell; NK; immunodeficiency; autoimmune disease; CSF;
XX	anti-tumour; ss.
XX	Synthetic.
OS	
XX	Key Location/Qualifiers
FH	misc_feature 7..12
FT	/tag= a
FT	/note= "palindrome, i.e. complementary strand sequence is identical reading 5'-3'."
FT	
FT	
XX	EP468520-A.
PN	
XX	
XX	29-JAN-1992.
PD	
XX	27-JUL-1990; 90JP-00197778.
PF	
XX	27-JUL-1990; 90JP-00197778.
PR	
XX	(MITK) MITSUI TOATSU CHEM INC.
PA	
PI	Tokunaga T, Kataoka T, Yamamoto S, Kuramoto E, Yano O, Shimada S;
PI	Makino T;
DR	WPI; 1992-034272/05.
XX	
XX	Immunostimulants contg. palindromic DNA - enhance interferon, macrophage activating factor and colony stimulating factor and promote lymphocyte proliferation.
PT	
PT	Claim 4; Page 22; 45pp; English.
XX	
XX	This single-stranded oligonucleotide is one example of an immunostimulatory sequence containing a palindrome. It increases mouse NK cell activity significantly more strongly than a control 45mer with no palindromic sequence. A fragment corresponding to nucleotides 1-30 of this sequence (i.e. contg. the palindrome) had a stronger effect on augmenting NK cell activity than nucleotides 16-45 fragment (i.e. lacking the palindrome). A fragment with nucleotides 1-30 but in which G(10) and T(11) were inverted (i.e. T(10), G(11) - no palindrome) had a weaker effect on increasing NK cell activity than the unchanged 1-30 sequence. The full-length 45mer containing the palindrome also induces CSF and has anti-tumour activity
CC	
CC	Sequence 45 BP; 8 A; 17 C; 15 G; 5 T; 0 U; 0 Other;
CC	
CC	Query Match 58.9%; Score 31.8; DB 2; Length 45;
CC	Best Local Similarity 94.3%; Pred. No. 0.061;
CC	Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 ACCGATGACGTGGCGGTGACGGCACCACGTCGC 35
Dd	1 ACCGATGACGTGGCGGTGACGGCACCACGCGC 35
RESULT 4	
AAF98882	
ID	AAF98882 standard; DNA; 45 BP.
XX	AAF98882;
XX	
XX	11-JUN-2001 (first entry)
DT	
XX	IFN-1 inducing protein cDNA fragment BCG-A4 SEQ ID NO: 163.
DE	Immunostimulatory nucleic acid; ISNA; human; interferon alpha; IFN-alpha;
KN	

Db 29 ACCGATGACGTCCCGGTGACGGCACCACGACGGC 63

RESULT 7

AAQ06507
ID AAQ06507 standard; DNA; 342 BP.

AC AAQ06507;

DT 25-MAR-2003 (revised)

DT 22-FEB-1991 (first entry)

XX Encodes protein IV homologous to mycobacterial antigen.

XX mycobacterial antigen; actinomycetales; ds.

XX Mycobacterium tuberculosis.

XX WO9012875-A.

XX 01-NOV-1990.

XX 17-APR-1989; 89FR-00005057.

XX 17-APR-1989; 89FR-00005057.

XX (INRM) INSERM INST NAT SANTE & RECH MED.

PA (INSP) INST PASTEUR.

XX Hance A, Grandchamp B, Levyfrebau V, Gicouel B;

XX WPI; 1990-348478/46.

XX Nucleotide sequences of actinomycetales - used as primers for synthesis
PT of DNA of actinomycetales.

XX Claim 9; Page 34; 61pp; French.

XX This sequence corresponds to the mycobacterial gene which encodes a 65KD
CC antigen of the group of tuberculosis bacteria. Regions within this
CC sequence can be used as primers to amplify mycobacterial genes and detect
CC mycobacteria. Antibodies can be induced by immunisation with the DNA
CC sequence or its fragments. These can also be used to detect mycobacteria
CC in assays such as ELISA or RIA procedures. See also AAQ06505-Q06506,
CC AAQ06508-Q06523 and AAR08336. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 342 BP; 75 A; 103 C; 122 G; 42 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 2; Length 342;
Best Local Similarity 94.3%; Pred. No. 0.081;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35

Db 46 ACCGATGACGTCCCGGTGACGGCACCACGACGGC 80

RESULT 8

ACF04267
ID ACF04267 standard; DNA; 604 BP.

AC ACF04267;

DT 06-NOV-2003 (first entry)

XX M bovis hsp65 gene fragment.

XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; gene; ds.

XX Mycobacterium bovis.

PN WO2003062470-A1.

PD 31-JUL-2003.

XX 21-JAN-2003; 2003WO-KR000131.

XX 24-JAN-2002; 2002KR-00004297.

PR 05-MAR-2002; 2002KR-00011648.

XX (BIOM-) BIOMEDLAB CORP.

PA (KIMB/) KIM B.

XX Kim B, Kook Y, Kim J;

XX WPI; 2003-598757/56.

XX Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.

XX Claim 3; Page 65; 102pp; English.

XX The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a gene fragment of the invention

XX Sequence 604 BP; 121 A; 182 C; 210 G; 91 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 9; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.088;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35

Db 56 ACCGATGACGTCCCGGTGACGGCACCACGACGGC 90

RESULT 9

ACF04273

ID ACF04273 standard; DNA; 604 BP.

XX ACF04273;

XX 06-NOV-2003 (first entry)

XX M microti hsp65 gene fragment.

XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; gene; ds.

XX Mycobacterium microti.

XX WO2003062470-A1.

XX 31-JUL-2003.

XX 21-JAN-2003; 2003WO-KR000131.

XX 24-JAN-2002; 2002KR-00004297.

PR 05-MAR-2002; 2002KR-00011648.

XX (BIOM-) BIOMEDLAB CORP.

PA (KIMB/) KIM B.

XX Kim B, Kook Y, Kim J;

XX WPI; 2003-598757/56.

PT Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.

XX PS Claim 3; Page 69-70; 102pp; English.

XX CC The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a gene fragment of the invention
XX SQ Sequence 604 BP; 121 A; 182 C; 210 G; 91 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 9; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.088;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACCGATGACGTCCGCGGTGACGCGACACACGTCGTC 35
|||||
DB 56 ACCGATGACGTCCGCGGTGACGCGACACACGCGC 90

RESULT 10

ACF04268
ID ACF04268 standard; DNA; 604 BP.

XX AC ACF04268;

DT 06-NOV-2003 (first entry)

XX M bovis BCG hsp65 gene fragment.

XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; gene; ds.

XX OS Mycobacterium bovis BCG.

XX PN WO2003062470-A1.

XX PD 31-JUL-2003.

XX PF 21-JAN-2003; 2003WO-KR000131.

XX PR 24-JAN-2002; 2002KR-00004297.

XX PR 05-MAR-2002; 2002KR-00011648.

XX PA (BIOM-) BIOMEDLAB CORP.

XX PA (KIMB/) KIM B.

XX PI Kim B, Kook Y, Kim J;

XX WPI; 2003-598757/56.

XX PT Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.

XX PS Claim 3; Page 65-66; 102pp; English.

XX CC The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a gene fragment of the invention
XX SQ Sequence 604 BP; 121 A; 182 C; 210 G; 91 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 9; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.088;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACCGATGACGTCCGCGGTGACGCGACACACGTCGTC 35
|||||
DB 56 ACCGATGACGTCCGCGGTGACGCGACACACGCGC 90

RESULT 11

ACF04263
ID ACF04263 standard; DNA; 604 BP.

XX AC ACF04263;

DT 06-NOV-2003 (first entry)

XX DE M africanum hsp65 gene fragment.

XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; gene; ds.

XX OS Mycobacterium africanum.

XX PN WO2003062470-A1.

XX PD 31-JUL-2003.

XX PF 21-JAN-2003; 2003WO-KR000131.

XX PR 24-JAN-2002; 2002KR-00004297.

XX PR 05-MAR-2002; 2002KR-00011648.

XX PA (BIOM-) BIOMEDLAB CORP.

XX PA (KIMB/) KIM B.

XX PI Kim B, Kook Y, Kim J;

XX WPI; 2003-598757/56.

XX PT Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.

XX PS Claim 3; Page 62; 102pp; English.

XX CC The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a gene fragment of the invention
XX SQ Sequence 604 BP; 121 A; 182 C; 210 G; 91 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 9; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.088;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACCGATGACGTCCGCGGTGACGCGACACACGTCGTC 35
|||||
DB 56 ACCGATGACGTCCGCGGTGACGCGACACACGCGC 90

RESULT 12

ACF04306
ID ACF04306 standard; DNA; 604 BP.

XX AC ACF04306;

XX XX

DT 06-NOV-2003 (first entry)
 XX M tuberculosis hsp65 gene fragment.
 XX Mycobacterium; hsp65; heat shock protein 65; identification;
 KW tuberculosis; gene; ds.
 XX Mycobacterium tuberculosis.
 OS
 XX WO2003062470-A1.
 PN 31-JUL-2003.
 XX 21-JAN-2003; 2003WO-KR000131.
 XX 24-JAN-2002; 2002KR-00004297.
 PR 05-MAR-2002; 2002KR-00011648.
 XX (BION-) BIOMEDLAB CORP.
 PA (KIMB/) KIM B.
 XX Kim B, Kook Y, Kim J;
 XX WPI; 2003-598757/56.
 XX Primers for amplifying a heat shock protein 65-gene fragment of
 PT mycobacterial species, useful for identifying and diagnosing
 PT mycobacterial species in tuberculosis infection.
 XX Claim 3; Page 93; 102pp; English.
 XX The present invention provides a pair of primers for specifically
 CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
 CC mycobacterial species comprising those sequences shown in ACF04316-
 CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
 CC mycobacterial species. The methods and compositions of the present
 CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
 CC and identifying and diagnosing mycobacterial species in tuberculosis
 CC infection. The present sequence is a gene fragment of the invention
 XX
 SQ Sequence 604 BP; 121 A; 182 C; 210 G; 91 T; 0 U; 0 Other;
 Query Match 58.9%; Score 31.8; DB 9; Length 604;
 Best Local Similarity 94.3%; Pred. No. 0.088; 2; Indels 0; Gaps 0;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ACCGATGACGTCCCGTGACGGCACCACGTCGTC 35
 Db 56 ACCGATGACGTCCCGTGACGGCACCACGTCGTC 90
 RESULT 13
 AAF25022
 ID AAF25022 standard; DNA; 888 BP.
 XX AAF25022;
 AC AAF25022;
 XX 30-APR-2001 (first entry)
 DT Nucleotide sequence of Hsp65-E7 fusion protein.
 DE Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein; ss.
 XX Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..888
 FT /tag= a
 FT /product= "Hsp65-E7 fusion protein"

XX WO200104344-A2.
 PN 18-JAN-2001.
 PD 10-JUL-2000; 2000WO-US018828.
 XX 08-JUL-1999; 99US-0143757P.
 PR (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX Siegel M, Chu NR, Mizzen LA;
 PI WPI; 2001-138361/14.
 XX P-PSDB; AAB31615.
 DR Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.
 XX Example 12; Fig 11; 88pp; English.
 XX The present sequence encodes a fusion protein comprising a Mycobacterium
 CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and
 CC then detecting the Th1-like response exhibited by the cell sample. The
 CC proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens
 XX SQ Sequence 888 BP; 224 A; 235 C; 272 G; 157 T; 0 U; 0 Other;
 Query Match 58.9%; Score 31.8; DB 5; Length 888;
 Best Local Similarity 94.3%; Pred. No. 0.093;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ACCGATGACGTCCCGTGACGGCACCACGTCGTC 35
 Db 238 ACCGATGACGTCCCGTGACGGCACCACGTCGTC 272
 RESULT 14
 ADW23618
 ID ADW23618 standard; DNA; 1496 BP.
 XX ADW23618;
 AC ADW23618;
 XX 10-MAR-2005 (first entry)
 DT HSP65 DNA.
 DE recombinant protein; vaccine; fusion protein; HSP65; ds.
 KW Unidentified.
 XX CN1462636-A.
 PN 24-DEC-2003.
 PD 30-MAY-2002; 2002CN-00122116.
 XX 30-MAY-2002; 2002CN-00122116.
 PR (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
 XX Wang L, Sun M, Yu Y;
 PI WPI; 2004-239553/23.
 XX

PT Vaccine of recombinant albumen for preventing and treating infection of
PT human hepatitis C virus.
PS Example 1; Page 14; 54pp; Chinese.
XX
XX The invention relates to a recombinant protein vaccine which is a fusion
CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
CC and nucleotide sequence for coding it, the expression carrier containing
CC nucleotide sequence, the host cell containing expression carrier, the
CC preparing process of recombinant protein vaccine, the vaccine containing
CC recombinant protein for preventing and treating hepatitis C and a method
CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a HSP65 DNA.
XX
SQ Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 13; Length 1496;
Best Local Similarity 94.3%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 35
DB 240 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 274
|||||

RESULT 15
ACA38272
ID ACA38272 standard; DNA; 1620 BP.
XX
AC ACA38272;
XX
XX 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #19929.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
XX Mycobacterium bovis.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU34402.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 26142; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;

Query Match 58.9%; Score 31.8; DB 8; Length 1620;
Best Local Similarity 94.3%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 35
DB 238 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 272
|||||

Search completed: May 4, 2006, 02:44:13
Job time : 409.241 secs

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no.	score	match	length	id	description
1	27.6	51.1	589	DN6064118	DN6064118 EST011629
2	27.6	51.1	584	DN606663	DN606663 EST011874
3	27.2	50.4	1911	BG859843	BG859843 1024065H0
4	27	50.0	410	CV956322	CV956322 PXRpxc_34
5	27	50.0	537	CV936508	CV936508 PMrpcm_60
6	27	50.0	543	CV931678	CV931678 PM057F4 m
7	27	50.0	553	CV943010	CV943010 PMrptc_69
8	27	50.0	551	CV939489	CV939489 PMrptc_10
9	27	50.0	562	CV913612	CV913612 PF019D2_8
10	27	50.0	576	CV931418	CV931418 PM054D9 m
11	27	50.0	605	CV901361	CV901361 PE051E6 m
12	27	50.0	618	CV941703	CV941703 PMrptc_42
13	27	50.0	625	CV937223	CV937223 PMrpcm_69
14	27	50.0	635	BE776273	BE776273 MY-13-B-0
15	27	50.0	637	BE777047	BE777047 MY-23-H-0
16	27	50.0	653	CF843128	CF843128 psHB023xN
17	27	50.0	658	CV956806	CV956806 PXRpxc_41
18	27	50.0	661	CV960823	CV960823 PYrpxc_24
19	27	50.0	662	CV958412	CV958412 PXRpxc_60
20	27	50.0	671	BE775585	BE775585 MY-04-C-0
21	27	50.0	677	CV893305	CV893305 PA003F9 m
22	27	50.0	676	CV940688	CV940688 PMrptc_28

```

Db      74 CGCGCGCGTTGACGGCGCGCGTGCACCTTTCCCGCTTGT 115
RESULT 2
DN606663      584 bp      mRNA      linear      EST 29-MAR-2005
LOCUS      EST01874 Sporophyte cDNA Library Porphyra haitanensis cDNA 5', mRNA
DEFINITION
ACCESSION      DN606663
VERSION      DN606663.1 GI:61664163
KEYWORDS
SOURCE
ORGANISM      Porphyra haitanensis
               Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
               Porphyra.
REFERENCE
AUTHORS      Fang, Y., Fan, X., Pang, G., Chen, B., Wang, G. and Hu, S.
TITLE      Sequencing and analysis of expressed sequence tags from a Porphyra
JOURNAL      Haitanensis Sporophyte cDNA Library
COMMENT      Unpublished (2005)
               Contact: Hu Songnian, Wang Guangce, Fang Yongjun, Fan Xiaolei, Pang
               Guoxing, Chen Baoxian
               Core Facilities (Hu); Key laboratory of experimental marine biology
               (Wang)
               Beijing Genomics Institute, CAS (Hu); Institute of oceanology, CAS
               (Wang)
               Beijing Airport Industrial Zone B-6, Beijing 101300, China (Hu);
               Nanhai Road 7#, Qingdao 266071, China (Wang)
               Tel: 86-10-80488851 (Hu); 86-532-2898574 (Wang)
               Fax: 86-10-80498676 (Hu); 86-532-2880645 (Wang)
               Email: hush@genomics.org.cn (Hu); gchwang@ms.qdio.ac.cn (Wang).
FEATURES
source
               1..584
               /organism="Porphyra haitanensis"
               /mol_type="mRNA"
               /db_xref="taxon:76159"
               /dev_stage="Sporophyte"
               /lab_host="DH108"
               /clone_lib="Sporophyte cDNA Library"
               /note="Vector: pBluescriptII"
ORIGIN
Query Match      51.1%; Score 27.6; DB 8; Length 584;
Best Local Similarity 78.6%; Pred. No. 12;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY      9 CTTGCGCGGTGACGGCACCGTGCCTGCTTTGTCGTTTGT 50
Db      75 CGCGCGCGTTGACGGCGCGCGTGCACCTTTCCCGCTTGT 116
RESULT 3
BG859843/c
LOCUS      BG859843
DEFINITION      1911 bp      mRNA      linear      EST 29-MAY-2001
               Chlamydomonas reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION      BG859843
VERSION      BG859843.1 GI:14241027
KEYWORDS
SOURCE
ORGANISM      Chlamydomonas reinhardtii
               Chlamydomonas reinhardtii
               Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
               Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE
AUTHORS      Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
               McDermott, J., Silflow, C., Stern, D. and Surzycki, R.
TITLE      Analyses of the Chlamydomonas reinhardtii Genome: A Model,
               Unicellular System for Analyzing Gene Function and Regulation in
               Vascular Plants; project phase 2
JOURNAL      Unpublished (2000)
COMMENT      Contact: Charles Hauser
               DCMB Box 91000
               Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
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/organism="Chlamydomonas reinhardtii"
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
ORIGIN
Query Match      50.4%; Score 27.2; DB 2; Length 1911;
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CV956322
LOCUS      CV956322
DEFINITION      410 bp      mRNA      linear      EST 25-JAN-2005
               Pxrpxc 3414 mycelium, starved in water Phytophthora infestans cDNA,
               mRNA sequence.
ACCESSION      CV956322.1 GI:58146113
VERSION      CV956322
KEYWORDS      EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM      Phytophthora infestans
               Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
               Phytophthora.
REFERENCE      1 (bases 1 to 410)
AUTHORS      Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C.,
               Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T.,
               Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, S.,
               Windass, J., Binder, A., Birch, P.R.J., Gisl, U., Govers, P., Gow, N.A.,
               Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,
               Lam, S.T. and Judelson, H.S.
TITLE      Large-scale gene discovery in the oomycete Phytophthora infestans
               reveals likely components of phytopathogenicity shared with true
               fungi
JOURNAL      Fungal Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED      15782637
COMMENT      Contact: Judelson HS
               Department of Plant Pathology
               University of California
               Webber Hall, Riverside, CA 92521, USA
               Tel: 909 787 4199
               Fax: 909 787 4294
               Email: howard.judelson@ucr.edu.
Location/Qualifiers
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CV936508      537 bp mRNA linear EST 25-JAN-2005
LOCUS      PMRpmc_6045 mating of 88069 (A1) and 618 (A2) Phytophthora
DEFINITION infestans cDNA, mRNA sequence.
ACCESSION CV936508
VERSION CV936508.1 GI:58126123
KEYWORDS EST.
SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 537)
AUTHORS Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
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Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

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Webster Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers

FEATURES
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RESULT 7
CV943010      553 bp mRNA linear EST 25-JAN-2005
LOCUS      PMRpmc_6963 mating of 88069 (A1) and 618 (A2) Phytophthora
DEFINITION infestans cDNA, mRNA sequence.
ACCESSION CV943010
VERSION CV943010.1 GI:58132766
KEYWORDS EST.
SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 553)
AUTHORS Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
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Email: howard.judelson@ucr.edu.
Location/Qualifiers

FEATURES
source
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Best Local Similarity 85.7%; Pred. No. 21;
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RESULT 6
CV931678      543 bp mRNA linear EST 25-JAN-2005
LOCUS      PM057P4 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
DEFINITION cDNA, mRNA sequence.
ACCESSION CV931678
VERSION CV931678.1 GI:58121298
KEYWORDS EST.

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Phytophthora infestans (potato late blight agent)
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 543)
AUTHORS Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
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Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers

FEATURES
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Best Local Similarity 85.7%; Pred. No. 21;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 35
|||||
Db 68 ACCACGACGGCGCGGTGACGGCACCACGTCGCG 102
|||||

RESULT 7
CV943010      553 bp mRNA linear EST 25-JAN-2005
LOCUS      PMRpmc_6963 mating of 88069 (A1) and 618 (A2) Phytophthora
DEFINITION infestans cDNA, mRNA sequence.
ACCESSION CV943010
VERSION CV943010.1 GI:58132766
KEYWORDS EST.
SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 553)
AUTHORS Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
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Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers

FEATURES
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Best Local Similarity 85.7%; Pred. No. 21;
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Qy 1 ACCGATGACGTGCGCGGTGACGGCACCACGTCGTC 35
|||||
Db 319 ACCACGACGGCGCGGTGACGGCACCACGTCGCG 353
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RESULT 6
CV931678      543 bp mRNA linear EST 25-JAN-2005
LOCUS      PM057P4 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
DEFINITION cDNA, mRNA sequence.
ACCESSION CV931678
VERSION CV931678.1 GI:58121298
KEYWORDS EST.

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Email: howard.judelson@ucr.edu.
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  Db 221 ACCAAGCAGCGCGCGGTGACGGCACCACGTCGCGC 255
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LOCUS
DEFINITION
  PMRpt 1071 mating of 88069 (A1) and 618 (A2) Phytophthora
  infestans cDNA, mRNA sequence.
ACCESSION
CV939489
VERSION
CV939489.1 GI:58129109
SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
  1 (bases 1 to 561)
    Randali,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
    Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
    Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
    Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
    Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
    Lam,S.T., and Judelson, H.S.
  Large-scale gene discovery in the oomycete Phytophthora infestans
  reveals likely components of phytopathogenicity shared with true
  fungi
  Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
COMMENT
  Contact: Judelson HS
  Department of Plant Pathology
  University of California
  Webber Hall, Riverside, CA 92521, USA
  Tel: 909 787 4199
  Fax: 909 787 4294
  Email: howard.judelson@ucr.edu.
FEATURES
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  Db 359 ACCAAGCAGCGCGCGGTGACGGCACCACGTCGCGC 393
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LOCUS
DEFINITION
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  cDNA, mRNA sequence.
ACCESSION
CV931418
VERSION
CV931418.1 GI:58121038
SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
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    Randali,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
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    Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
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    Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
    Lam,S.T., and Judelson, H.S.
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  Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
COMMENT
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  Webber Hall, Riverside, CA 92521, USA
  Tel: 909 787 4199
  Fax: 909 787 4294
  Email: howard.judelson@ucr.edu.
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LOCUS
DEFINITION
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  sequence.
ACCESSION
CV9313612
VERSION
CV9313612.1 GI:58103161
SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
  1 (bases 1 to 562)
    Randali,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
    Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
    Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
    Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
    Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
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  Fax: 909 787 4294
  Email: howard.judelson@ucr.edu.
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  Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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  Db 359 ACCAAGCAGCGCGCGGTGACGGCACCACGTCGCGC 393
RESULT 10
CV931418
LOCUS
DEFINITION
  PM054D9 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
  cDNA, mRNA sequence.
ACCESSION
CV931418
VERSION
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SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
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    Randali,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
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    Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
    Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
    Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
    Lam,S.T., and Judelson, H.S.
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15782637
COMMENT
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  Tel: 909 787 4199
  Fax: 909 787 4294
  Email: howard.judelson@ucr.edu.
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  Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  QY 1 ACCGATGAGTCGCGCGGTGACGGCACCACGTCGTC 35
  Db 384 ACCAAGCAGCGCGCGGTGACGGCACCACGTCGCGC 418
RESULT 9
CV939489
LOCUS
DEFINITION
  PMRpt 1071 mating of 88069 (A1) and 618 (A2) Phytophthora
  infestans cDNA, mRNA sequence.
ACCESSION
CV939489
VERSION
CV939489.1 GI:58129109
SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
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    Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
    Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
    Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
    Lam,S.T., and Judelson, H.S.
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  Db 384 ACCAAGCAGCGCGCGGTGACGGCACCACGTCGCGC 418
RESULT 9

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Windass, J., Binder, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A., Mauch, P., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S., Lam, S.T., and Judelson, H.S.
Large-scale gene discovery in the oomycete *Phytophthora infestans* reveals likely components of phytopathogenicity shared with true fungi

JOURNAL PUBLISHED

Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

15782637

Contact: Judelson HS

Department of Plant Pathology

University of California

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Fax: 909 787 4294

Email: howard.judelson@ucr.edu.

FEATURES

source

1. .625
Location/Qualifiers
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/strain="88069 and 618"
/db_xref="taxon:4787"
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/note="Vector: pSPORT1"

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Db 332 ACCAACGACGCGCGCGTGACGGCACCACGTCGCGC 366

RESULT 14

BE776273

LOCUS

MY-13-B-06 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.

BE776273

ACCESSION

BE776273.1 GI:10229928

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

Contact: Govers F
Laboratory of Phytopathology
Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
Location/Qualifiers
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/organism="Phytophthora infestans"
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/lab_host="E. coli, strain DH5-alpha"
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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Total RNA was isolated from mycelium of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded

FEATURES

source

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Location/Qualifiers
/organism="Phytophthora infestans"
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ORIGIN

Query Match 50.0%; Score 27; DB 2; Length 635;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 329 ACCAACGACGCGCGCGTGACGGCACCACGTCGCGC 363

RESULT 15

BE777047

LOCUS

MY-23-H-09 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.

BE777047

ACCESSION

BE777047.1 GI:10230702

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

Contact: Govers F
Laboratory of Phytopathology
Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
Location/Qualifiers
1. .637
/organism="Phytophthora infestans"
/mol_type="mRNA"
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/clone_lib="PinfestansMY"
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FEATURES

source

1. .637
Location/Qualifiers
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/dev_stage="4-week old vegetative, non-sporulating mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/clone_lib="PinfestansMY"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Total RNA was isolated from mycelium of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelial) and the successive number of the microtiter plate (e.g. MY-06-A-04)."

ORIGIN

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Best Local Similarity 85.7%; Pred. No. 21;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35

|||||

Db 329 ACCAACGACGCGCGCGTGACGGCACCACGTCGCGC 363

Search completed: May 4, 2006, 07:17:30

Job time : 3832.48 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 114.207 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-7
Perfect score: 54
Sequence: 1 accgatgacgtcgccgtga.....cgtttgcgtttgtcggtt 54

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgm2_6/ptodata/1/ina/5 COMB.seq.*
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4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/1/ina/H COMB.seq.*
6: /cgm2_6/ptodata/1/ina/PCTUS COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	58.9	45	3	US-09-672-126B-163
2	31.8	58.9	268	2	US-08-105-168B-1
3	31.8	58.9	268	2	US-08-105-168B-2
4	31.8	58.9	268	2	US-08-698-948-1
5	31.8	58.9	268	2	US-08-698-948-2
6	31.8	58.9	314	2	US-08-105-168B-23
7	31.8	58.9	314	2	US-08-698-948-23
8	31.8	58.9	342	2	US-08-473-020A-31
9	31.8	58.9	343	2	US-08-473-020A-4
10	31.8	58.9	350	2	US-08-105-168B-22
11	31.8	58.9	350	2	US-08-698-948-22
12	31.8	58.9	888	3	US-09-613-303-32
13	31.8	58.9	888	3	US-10-267-311-32
14	31.8	58.9	1623	3	US-09-613-303-3
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16	31.8	58.9	1623	3	US-09-712-363-23
17	31.8	58.9	1920	3	US-09-613-303-16
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19	31.8	58.9	1947	3	US-09-613-303-28
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21	31.8	58.9	2073	3	US-10-068-059-9
22	31.8	58.9	2175	3	US-10-068-059-7
23	31.8	58.9	2175	3	US-10-068-059-11
24	31.8	58.9	2241	3	US-10-068-059-5

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27	31.8	58.9	4380	3	US-08-955-565A-3
28	31.8	58.9	4403765	3	US-09-103-840A-2
29	31.8	58.9	4411529	3	US-09-103-840A-1
30	30.2	55.9	268	2	US-08-105-168B-3
31	30.2	55.9	268	2	US-08-698-948-3
32	30	55.6	30	3	US-09-690-921-3
33	30	55.6	30	3	US-09-301-829A-3
34	30	55.6	30	3	US-09-672-126B-164
35	28.6	53.0	268	2	US-08-105-168B-7
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39	28.6	53.0	343	2	US-08-473-020A-3
40	27	50.0	268	2	US-08-105-168B-5
41	27	50.0	268	2	US-08-698-948-5
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44	25.4	47.0	19954	3	US-09-902-540-1150
45	24.4	45.2	26	2	US-08-429-121B-49

ALIGNMENTS

RESULT 1
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; Sequence 163, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-163

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Best Local Similarity	94.3%	Pred. No. 0.011;		
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				Gaps 0;

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US-08-105-168B-1
; Sequence 1, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION
; OF MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300

;
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium bovis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-105-168B-1
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Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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US-08-105-168B-2
; Sequence 2, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536

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; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium microti
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 461-728
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-105-168B-2
;
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Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
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RESULT 4
US-08-698-948-1
; Sequence 1, Application US/08698948
; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium bovis
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY: 461-728
LOCATION: 461-728
IDENTIFICATION METHOD:
OTHER INFORMATION:

US-08-698-948-1

Query Match 58.9%; Score 31.8; DB 2; Length 268;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 35
Db 29 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 63

RESULT 5
US-08-698-948-2
Sequence 2, Application US/08698948
Patent No. 5849901
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948
FILING DATE: August 16, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium microti
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY: 461-728
LOCATION: 461-728
IDENTIFICATION METHOD:
OTHER INFORMATION:

US-08-698-948-2

Query Match 58.9%; Score 31.8; DB 2; Length 268;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 35
Db 29 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 63

RESULT 6
US-08-105-168B-23
Sequence 23, Application US/08105168B
Patent No. 5589585
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28835
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE: Mycobacterium tuberculosis
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 438-751
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-105-1688-23

Query Match 58.9%; Score 31.8; DB 2; Length 314;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCGGTGACGGCACCACGTCGTC 35
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DB 52 ACCGATGACGTCCGGTGACGGCACCACGTCGTC 86

RESULT 7
US-08-698-948-23
Sequence 23, Application US/08698948
Patent No. 5849901
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948
FILING DATE: August 16, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-6400

TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE: Mycobacterium tuberculosis
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 438-751
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-23

Query Match 58.9%; Score 31.8; DB 2; Length 314;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCGGTGACGGCACCACGTCGTC 35
|||||
DB 52 ACCGATGACGTCCGGTGACGGCACCACGTCGTC 86

RESULT 8
US-08-473-020A-31
Sequence 31, Application US/08473020A
Patent No. 587273
GENERAL INFORMATION:
APPLICANT: Hance, Allan J
APPLICANT: Grandchamp-Desraux, Bernard
APPLICANT: Levy-Frebault, Veronique
APPLICANT: Gicquel, Brigitte
TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
TITLE OF INVENTION: applications to the synthesis or detection of nucleic
TITLE OF INVENTION: acids, products of expression of such sequences and
TITLE OF INVENTION: application as immunogenic compositions.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,020A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249

```

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-020A-31

Query Match 58.9%; Score 31.8; DB 2; Length 342;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 35
    |||||||
Db 46 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 80
    |||||||

RESULT 9
US-08-473-020A-4
; Sequence 4, Application US/08473020A
; Patent No. 587273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Gicquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,020A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/623,729
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H
; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-020A-4

Query Match 58.9%; Score 31.8; DB 2; Length 343;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 35
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```

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Db 47 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 81

RESULT 10
US-08-105-168B-22
; Sequence 22, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 438-787
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-22

Query Match 58.9%; Score 31.8; DB 2; Length 350;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 35
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Db 52 ACCGATGACGTGCGCGGTGACGGCACCGTCGTC 86
    |||||||

RESULT 11
US-08-698-948-22
; Sequence 22, Application US/08698948

```

; Patent No. 5849901
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,948
; FILING DATE: August 16, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,168
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 438-787
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-698-948-22

Query Match 58.9%; Score 31.8; DB 2; Length 350;
Best Local Similarity 94.3%; Pred. No. 0.015;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
|||||
Db 52 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 86

RESULT 12
US-09-613-303-32
; Sequence 32, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin

; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-09-613-303-32

Query Match 58.9%; Score 31.8; DB 3; Length 888;
Best Local Similarity 94.3%; Pred. No. 0.018;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
|||||
Db 238 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 272

RESULT 13
US-10-267-311-32
; Sequence 32, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match 58.9%; Score 31.8; DB 3; Length 888;
Best Local Similarity 94.3%; Pred. No. 0.018;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
|||||
Db 238 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 272

RESULT 14
US-09-613-303-3
; Sequence 3, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin

; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-09-613-303-3

Query Match 58.9%; Score 31.8; DB 3; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 35
|||||
Db 238 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 272

RESULT 15
US-10-267-311-3
; Sequence 3, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 58.9%; Score 31.8; DB 3; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 35
|||||
Db 238 ACCGATGACGTCGCGGTGACGGCACCACGTCGTC 272

Search completed: May 4, 2006, 07:23:47
Job time : 119.207 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 07:24:16 ; Search time 806.897 Seconds
(without alignments)
553.412 Million cell updates/sec

Title: US-10-789-758A-7
Perfect score: 54
Sequence: 1 accgatgacgtcgccgtga.....cgtttgtcgtttgtcgtt 54

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	54	8	US-10-789-758-7
2	31.8	58.9	45	10	US-11-056-463-163
3	31.8	58.9	604	8	US-10-500-586-2
4	31.8	58.9	604	8	US-10-500-586-6
5	31.8	58.9	604	8	US-10-500-586-7
6	31.8	58.9	604	8	US-10-500-586-12
7	31.8	58.9	604	8	US-10-500-586-45
8	31.8	58.9	888	5	US-10-267-311-32
9	31.8	58.9	888	9	US-10-679-956-32
10	31.8	58.9	1620	7	US-10-282-122A-26142
11	31.8	58.9	1623	7	US-09-712-363-23
12	31.8	58.9	1623	5	US-10-267-311-3
13	31.8	58.9	1623	7	US-10-282-122A-28196
14	31.8	58.9	1623	9	US-10-679-956-3
15	31.8	58.9	1761	8	US-10-635-211-1
16	31.8	58.9	1920	5	US-10-267-311-16
17	31.8	58.9	1920	5	US-10-679-956-16
18	31.8	58.9	1947	5	US-10-267-311-28
19	31.8	58.9	1947	9	US-10-679-956-28
20	31.8	58.9	2073	5	US-10-068-059-9
21	31.8	58.9	2073	9	US-10-941-049-9
22	31.8	58.9	2130	9	US-10-068-059-7
23	31.8	58.9	2130	9	US-10-941-049-7

24	31.8	58.9	2175	5	US-10-068-059-11	Sequence 11, Appl
25	31.8	58.9	2175	9	US-10-941-049-11	Sequence 11, Appl
26	31.8	58.9	2241	5	US-10-068-059-5	Sequence 5, Appl
27	31.8	58.9	2241	9	US-10-941-049-5	Sequence 5, Appl
28	31.8	58.9	2847	5	US-10-267-311-20	Sequence 20, Appl
29	31.8	58.9	2847	9	US-10-679-956-20	Sequence 20, Appl
30	31.8	58.9	86114	6	US-10-080-170-648	Sequence 648, App
31	31.8	58.9	86114	7	US-10-080-170-648	Sequence 648, App
32	31.8	58.9	86114	8	US-10-468-356-648	Sequence 648, App
33	30.2	55.9	604	8	US-10-500-586-18	Sequence 18, Appl
34	30.2	55.9	604	8	US-10-500-586-39	Sequence 39, Appl
35	30	55.6	30	5	US-10-011-635A-6	Sequence 6, Appl
36	30	55.6	30	6	US-10-304-616-4	Sequence 4, Appl
37	30	55.6	30	6	US-10-379-164-3	Sequence 3, Appl
38	30	55.6	30	6	US-10-233-902-7	Sequence 7, Appl
39	30	55.6	30	7	US-10-399-356-3	Sequence 3, Appl
40	30	55.6	30	7	US-10-333-448-3	Sequence 3, Appl
41	30	55.6	30	8	US-10-478-188-3	Sequence 3, Appl
42	30	55.6	30	8	US-10-899-771-26	Sequence 26, Appl
43	30	55.6	30	9	US-10-894-655-4	Sequence 4, Appl
44	30	55.6	30	10	US-11-056-463-164	Sequence 164, App
45	30	55.6	30	10	US-11-041-636-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-789-758-7
; Sequence 7, Application US/10789758
; Publication No. US20050002958A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Joe
; APPLICANT: Garcon, Nathalie
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45187
; CURRENT FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/10/018,704
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/EP00/05841
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: GB 9915204.3
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing a CpG motif
US-10-789-758-7
Query Match 100.0%; Score 54; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGATGACGTGCGCGGTGACGGACCGACGTCGTCGTTTGTGCGTTTGTGCGTT 54
DB 1 ACCGATGACGTGCGCGGTGACGGACCGACCGTCGTCGTTTGTGCGTTTGTGCGTT 54
RESULT 2
US-11-056-463-163
; Sequence 163, Application US/11056463
; Publication No. US20050169888A1
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory

```
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039.70044US01
; CURRENT APPLICATION NUMBER: US/11/056,463
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 09/672,126
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,147
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-11-056-463-163
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Query Match          58.9%; Score 31.8; DB 10; Length 45;
Best Local Similarity 94.3%; Pred. No. 0.022; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ACCGATGACGTCCCGGTGACGGCACCACCGTCGTC 35
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Db 1 ACCGATGACGTCCCGGTGACGGCACCACCGCGC 35
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RESULT 3

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US-10-500-586-2
; Sequence 2, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
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; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-10-500-586-2
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Query Match          58.9%; Score 31.8; DB 8; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.029; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ACCGATGACGTCCCGGTGACGGCACCACCGTCGTC 35
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Db 56 ACCGATGACGTCCCGGTGACGGCACCACCGCGC 90
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RESULT 4

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US-10-500-586-6
; Sequence 6, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
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; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
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; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-500-586-6
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Query Match          58.9%; Score 31.8; DB 8; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.029; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ACCGATGACGTCCCGGTGACGGCACCACCGTCGTC 35
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Db 56 ACCGATGACGTCCCGGTGACGGCACCACCGCGC 90
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RESULT 5

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US-10-500-586-7
; Sequence 7, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
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; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 7
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-10-500-586-7
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Query Match          58.9%; Score 31.8; DB 8; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.029; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ACCGATGACGTCCCGGTGACGGCACCACCGTCGTC 35
      |||||
Db 56 ACCGATGACGTCCCGGTGACGGCACCACCGCGC 90
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RESULT 6

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US-10-500-586-12
; Sequence 12, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
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; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
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; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 12
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Mycobacterium microti
US-10-500-586-12

Query Match      58.9%; Score 31.8; DB 8; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.029;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 56 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 90
    |||||

RESULT 7
US-10-500-586-45
; Sequence 45, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIES
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 45
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-500-586-45

Query Match      58.9%; Score 31.8; DB 8; Length 604;
Best Local Similarity 94.3%; Pred. No. 0.029;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 56 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 90
    |||||

RESULT 8
US-10-267-311-32
; Sequence 32, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match      58.9%; Score 31.8; DB 5; Length 888;
Best Local Similarity 94.3%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 272
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RESULT 9
US-10-679-956-32
; Sequence 32, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-679-956-32

Query Match      58.9%; Score 31.8; DB 9; Length 888;
Best Local Similarity 94.3%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 272
    |||||

RESULT 10
US-10-282-122A-26142
; Sequence 26142, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26142
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-36142

Query Match          58.9%; Score 31.8; DB 7; Length 1620;
Best Local Similarity 94.3%; Pred. No. 0.032; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCCCGGTGACGGCACCACGCGC 272

RESULT 11
US-09-712-363-23
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match          58.9%; Score 31.8; DB 3; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.032; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCCCGGTGACGGCACCACGCGC 272

RESULT 12
US-10-267-311-3
; Sequence 3, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match          58.9%; Score 31.8; DB 5; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.032; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2;

QY 1 ACCGATGACGTCCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCCCGGTGACGGCACCACGCGC 272

RESULT 13
US-10-282-122A-28196
; Sequence 28196, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28196
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28196

Query Match      58.9%; Score 31.8; DB 7; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.032;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
    |||||
Db 238 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 272

RESULT 14
US-10-679-956-3
; Sequence 3, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-679-956-3

Query Match      58.9%; Score 31.8; DB 9; Length 1623;
Best Local Similarity 94.3%; Pred. No. 0.032;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
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Db 238 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 272

RESULT 15
US-10-635-211-1
; Sequence 1, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1761)
US-10-635-211-1

Query Match      58.9%; Score 31.8; DB 8; Length 1761;
Best Local Similarity 94.3%; Pred. No. 0.032;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCCGGTGACGGCACCACGTCGTC 35
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Db 238 ACCGATGACGTCGCCGGTGACGGCACCACGACGGC 272

Search completed: May 4, 2006, 09:01:03
Job time : 808.897 secs
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Title: US-10-789-758A-7
Perfect score: 54
Sequence: 1 accgatgacgtcgccgtga.....cgtttgcgtttgttgcgtt 54
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9306428 seqs, 2036268586 residues
Total number of hits satisfying chosen parameters: 18612856
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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					19: /SIDS5/prodata/2/pubpna/US60_NEW_PUB.seq:*				

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17	24	44.4	24	17	US-11-127-654-399	Sequence 399, App
18	24	44.4	24	17	US-11-127-654-922	Sequence 922, App
19	24	44.4	24	17	US-11-061-140-285	Sequence 285, App
20	24	44.4	24	17	US-11-061-140-334	Sequence 334, App
21	24	44.4	24	17	US-11-154-324-5	Sequence 5, Appli
22	24	44.4	24	17	US-11-107-364-26	Sequence 26, Appli
23	24	44.4	24	17	US-11-019-955-3	Sequence 3, Appli
24	24	44.4	24	17	US-11-114-325-9	Sequence 9, Appli
25	24	44.4	24	17	US-11-183-253-2	Sequence 2, Appli
26	24	44.4	24	17	US-11-183-253-8	Sequence 8, Appli
27	24	44.4	24	17	US-11-099-683-54	Sequence 54, Appli
28	24	44.4	24	17	US-11-184-065A-1	Sequence 1, Appli
29	24	44.4	25	17	US-11-127-654-862	Sequence 862, App
30	24	44.4	29	17	US-11-127-654-295	Sequence 295, App
31	24	44.4	32	17	US-11-127-654-411	Sequence 411, App
32	24	44.4	1339	13	US-10-703-799B-7	Sequence 7, Appli
33	24	44.4	1737	13	US-10-703-799B-5	Sequence 5, Appli
34	23	42.6	23	10	US-10-619-279-123	Sequence 123, App
35	23	42.6	23	11	US-10-533-634-31	Sequence 31, Appl
36	23	42.6	23	12	US-10-382-822-123	Sequence 123, App
37	23	42.6	23	17	US-11-127-654-398	Sequence 398, App
38	23	42.6	23	18	US-11-151-123-1	Sequence 1, Appli
c	39	22.6	41.9	1720	US-10-216-488-1	Sequence 1, Appli
	40	22.4	41.5	24	US-11-127-654-332	Sequence 332, App
	41	22.4	41.5	24	US-11-183-253-5	Sequence 5, Appli
c	42	22.4	41.5	24	US-11-099-683-143	Sequence 143, App
	43	22	40.7	365	US-09-925-065A-63350	Sequence 63350, A
	44	22	40.7	365	US-10-301-480-164588	Sequence 164588,
c	45	22	40.7	365	US-10-301-480-777997	Sequence 777997,

ALIGNMENTS

RESULT 1
US-10-469-561-7
; Sequence 7, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469.561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-7

Query Match 55.6%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGATGACGTCGCCGGTGACGGCACCACG 30
Db 1 ACCGATGACGTCGCCGGTGACGGCACCACG 30

RESULT 2
US-10-741-720A-25
; Sequence 25, Application US/10741720A
; Publication No. US20060058254A1
; GENERAL INFORMATION:

```
; APPLICANT: DINA, Dino
; APPLICANT: FEARON, Karen L.
; APPLICANT: MARSHALL, Jason
; TITLE OF INVENTION: IMMUNOSTIMULATORY SEQUENCE
; FILE REFERENCE: 377882003300
; CURRENT APPLICATION NUMBER: US/10/741,720A
; PRIOR FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/436,122
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/447,885
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/467,546
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-741-720A-25

Query Match          49.6%; Score 26.8; DB 12; Length 30;
Best Local Similarity 93.3%; Pred. No. 0.31;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCACG 30
    ||||| ||||| ||||| ||||| |||||
Db 1 ACCGATAACGTTGCCGGTGACGGCACCACG 30

RESULT 3
US-10-741-720A-92
; Sequence 92, Application US/10741720A
; Publication No. US20060058254A1
; GENERAL INFORMATION:
; APPLICANT: DINA, Dino
; APPLICANT: FEARON, Karen L.
; APPLICANT: MARSHALL, Jason
; TITLE OF INVENTION: IMMUNOSTIMULATORY SEQUENCE
; FILE REFERENCE: 377882003300
; CURRENT APPLICATION NUMBER: US/10/741,720A
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/436,122
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/447,885
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/467,546
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-741-720A-92

Query Match          49.6%; Score 26.8; DB 12; Length 30;
Best Local Similarity 93.3%; Pred. No. 0.31;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGATGACGTGCGCGGTGACGGCACCACG 30
    ||||| ||||| ||||| ||||| |||||
Db 1 ACCGATAACGTTGCCGGTGACGGCACCACG 30

RESULT 4
US-10-835-475-8
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; Sequence 8, Application US/10835475
; Publication No. US20050244410A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: Toll-Like Receptor Binding Agents and Uses Thereof
; FILE REFERENCE: CEN5022 USNP
; CURRENT APPLICATION NUMBER: US/10/835,475
; CURRENT FILING DATE: 2004-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligodinucleotide
US-10-835-475-8

Query Match          44.4%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
    ||||| ||||| ||||| ||||| |||||
Db 1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 5
US-10-497-591A-22
; Sequence 22, Application US/10497591A
; Publication No. US20050250716A1
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, WALTER
; APPLICANT: SCHELLACK, CAROLA
; APPLICANT: EGYED, ALENA
; APPLICANT: LINGNAU, KAREN
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGODEOXYNUCLEOTIDES
; FILE REFERENCE: SONN:045US
; CURRENT APPLICATION NUMBER: US/10/497,591A
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: PCT/EP02/13791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: A 1924/2001
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-497-591A-22

Query Match          44.4%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
    ||||| ||||| ||||| ||||| |||||
Db 1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 6
US-10-469-561-8
; Sequence 8, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
```

```
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 24
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-8

Query Match      44.4%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
Db      1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 7
US-10-619-279-46
; Sequence 46, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-46

Query Match      44.4%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
Db      1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 8
US-10-382-822-46
; Sequence 46, Application US/10382822
; Publication No. US20060058251A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; FILE REFERENCE: C01039,70062,US
; CURRENT APPLICATION NUMBER: US/10/382,822
; CURRENT FILING DATE: 2003-03-06
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; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-382-822-46

Query Match      44.4%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
Db      1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 9
US-10-741-720A-3
; Sequence 3, Application US/10741720A
; Publication No. US20060058254A1
; GENERAL INFORMATION:
; APPLICANT: DINA, Dino
; APPLICANT: FEARON, Karen L.
; APPLICANT: MARSHALL, Jason
; TITLE OF INVENTION: IMMUNOSTIMULATORY SEQUENCE
; FILE REFERENCE: 377882003300
; CURRENT APPLICATION NUMBER: US/10/741,720A
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/436,122
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/447,885
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/467,546
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-741-720A-3

Query Match      44.4%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 TCGTCGTTTTCGTTTTCGTTTTCGTT 54
Db      1 TCGTCGTTTTCGTTTTCGTTTTCGTT 24

RESULT 10
US-11-127-654-238
; Sequence 238, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
```

```
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-238

Query Match      44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24

RESULT 11
US-11-127-654-253
; Sequence 253, Application US/11/127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-253

Query Match      44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24

RESULT 12
US-11-127-654-290
; Sequence 290, Application US/11/127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-294

Query Match      44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24
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; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-290

Query Match      44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24

RESULT 13
US-11-127-654-294
; Sequence 294, Application US/11/127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-294

Query Match      44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 54
```


Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24

RESULT 14
US-11-127-654-341
; Sequence 341, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 341
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: biotinylated
US-11-127-654-341

Query Match 44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24

RESULT 15
US-11-127-654-343
; Sequence 343, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 343
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2)..(2)
; OTHER INFORMATION: m5C
US-11-127-654-343

Query Match 44.4%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 31 TCGTCGTTTGTGCGTTTGTGCGTT 54
Db 1 TCGTCGTTTGTGCGTTTGTGCGTT 24
Search completed: May 4, 2006, 10:07:23
Job time : 1233.38 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 01:23:12 ; Search time 150.46 Seconds
(without alignments)
885.910 Million cell updates/sec

Title: US-10-789-758a-1

Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	AAV60950 Unmethyla
2	20	100.0	20	2	AAV47683 Unmethyla
3	20	100.0	20	2	AAV27667 Immunosti
4	20	100.0	20	2	AAZ41946 IL-12 sec
5	20	100.0	20	2	AAZ41949 IL-12 sec
6	20	100.0	20	2	AAZ78802 HPV fusio
7	20	100.0	20	2	AAZ31943 Cpg adjuv
8	20	100.0	20	2	AAV74237 Cpg-N mot
9	20	100.0	20	2	AAV74244 Cpg-N mot
10	20	100.0	20	2	AAV74242 Cpg-N mot
11	20	100.0	20	2	AAZ88536 Cytosine-
12	20	100.0	20	2	AAZ28191 Chlamydia
13	20	100.0	20	3	AAZ61012 Nucleotid
14	20	100.0	20	3	AAZ61010 Nucleotid
15	20	100.0	20	3	AAZ48025 Immune re
16	20	100.0	20	3	AAZ48022 Immune re
17	20	100.0	20	3	AAZ47885 Immunosti
18	20	100.0	20	3	AAZ47887 Immunosti
19	20	100.0	20	3	AAZ90447 Cpg adjuv

20	20	100.0	20	3	AAZ99174	AAZ99174 Inflammat
21	20	100.0	20	3	AAZ99004	AAZ99004 Cpg motif
22	20	100.0	20	3	AAZ47601	AAZ47601 Murine im
23	20	100.0	20	3	AAZ60277	AAZ60277 Immunosti
24	20	100.0	20	3	AAZ64136	AAZ64136 Immunosti
25	20	100.0	20	4	AAH20390	AAH20390 Cpg motif
26	20	100.0	20	4	AAH20392	AAH20392 Cpg motif
27	20	100.0	20	4	AAH50580	AAH50580 Cpg motif
28	20	100.0	20	4	AAH19260	AAH19260 Cpg oligo
29	20	100.0	20	4	AAAF98805	AAAF98805 Cpg immun
30	20	100.0	20	4	AAAF59506	AAAF59506 Immunosti
31	20	100.0	20	4	AAAF59501	AAAF59501 Immunosti
32	20	100.0	20	4	AAAC82106	AAAC82106 Oligonucle
33	20	100.0	20	4	AAAF99748	AAAF99748 Immunosti
34	20	100.0	20	4	AAAF99745	AAAF99745 Immunosti
35	20	100.0	20	4	AAAF98944	AAAF98944 Immunosti
36	20	100.0	20	4	AAAF99752	AAAF99752 Immunosti
37	20	100.0	20	4	AAAF99175	AAAF99175 Immunosti
38	20	100.0	20	4	AAAF99750	AAAF99750 Immunosti
39	20	100.0	20	4	AAAF99744	AAAF99744 Immunosti
40	20	100.0	20	4	AAAF99751	AAAF99751 Immunosti
41	20	100.0	20	4	AAAF99012	AAAF99012 Immunosti
42	20	100.0	20	4	AAAF99746	AAAF99746 Immunosti
43	20	100.0	20	4	AAAF99753	AAAF99753 Immunosti
44	20	100.0	20	4	AAAF99817	AAAF99817 Immunosti
45	20	100.0	20	4	AAAF99749	AAAF99749 Immunosti

ALIGNMENTS

RESULT 1

AAV60950

ID AAV60950 standard; DNA; 20 BP.

AC AAV60950;

DT 14-DEC-1998 (first entry)

DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.

KW ss; unmethylated CpG dinucleotide; immune response; natural killer cell;

KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.

OS Synthetic.

PN WO9840100-A1.

XX 17-SEP-1998.

PF 10-MAR-1998; 98WO-US004703.

PR 10-MAR-1997; 97US-0040376P.

XX (OTTA-) OTTAWA CIVIC LOEB RES INST.

PA (QIAG-) QIAGEN GMBH.

XX (IOWA) UNIV IOWA RES FOUND.

PI Davis HL, Schorr J, Krieg AM;

XX WPI, 1998-520792/44.

DR Use of oligonucleotides containing an unmethylated CpG dinucleotide -
useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
for inducing immune response in subject.

XX Claim 14; Page 35; 67pp; English.

PS Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
affect the immune response in a subject by activating natural killer
cells or redirecting a subject's immune response from a Th2 to a Th1
response by inducing monocytic and other cells to produce Th1 cytokines.
These nucleic acids containing at least 1 unmethylated CpG can be used as

CC an adjuvant, specifically to induce an immune response against an
 CC antigenic protein, and are used particularly for virally mediated
 CC disorders, e.g. hepatitis B virus infection
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTGACGTT 20
 DB 1 TCCATGACGTTCTGACGTT 20
 RESULT 2
 AAV47683
 ID AAV47683 standard; DNA; 20 BP.
 XX
 AC AAV47683;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Unmethylated CpG dinucleotide 1826.
 XX
 KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KW pulmonary disorder; asthma; environmentally induced airway disease;
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KW inflammatory bowel disease; ss.
 XX
 OS Synthetic.
 XX
 PN WO9837919-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 25-FEB-1998; 98WO-US003678.
 XX
 PR 28-FEB-1997; 97US-0039405P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Schwartz DA, Krieg AM;
 XX
 DR WPI; 1998-480941/41.
 XX
 PT Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow or
 PT inhibiting an inflammatory response.
 XX
 PS Claim 35; Page 27; 65pp; English.
 XX
 CC This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an
 CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with Gram-
 CC positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTGACGTT 20
 DB 1 TCCATGACGTTCTGACGTT 20
 RESULT 3
 AAV27667
 ID AAV27667 standard; DNA; 20 BP.
 XX
 AC AAV27667;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Immunostimulatory oligodeoxyribonucleotide of the invention.
 XX
 KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
 KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
 KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
 KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9818810-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 30-OCT-1997; 97WO-US019791.
 XX
 PR 30-OCT-1996; 96US-00738652.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Krieg AM, Kline JN;
 XX
 DR WPI; 1998-272127/24.
 XX
 PT New immunostimulatory nucleic acid molecules - which contain at least one
 PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
 PT or autoimmune disease.
 XX
 PS Claim 35; Page 84; 109pp; English.
 XX
 CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
 CC of the invention. The ODNs contain at least one unmethylated CpG
 CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
 CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
 CC thymine, X2 is cytosine or thymine, N1 is any nucleotide and N1+N2 is 0-26
 CC bases with the provision that N1 and N2 does not contain a CCG tetramer
 CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
 CC one nucleotide separates consecutive CpGs, X1 and X2 are selected from
 CC GpT, GpG, GpA, Apt and Apg, X3 and X4 are selected from Tpt or Cpt, N1 is
 CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
 CC does not contain a CCG tetramer or more than one CCG or CCG trimer. The
 CC ODNs activate lymphocytes in a subject and redirect a subject's immune
 CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other
 CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
 CC The ODNs can be used to treat or prevent an asthmatic disorder,
 CC autoimmune diseases, in desensitisation therapy, as an artificial
 CC adjuvant during antibody generation in a mammal such as a mouse or a
 CC human
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTGACGTT 20
 DB 1 TCCATGACGTTCTGACGTT 20

RESULT 4
AAZ41946
ID AAZ41946 standard; DNA; 20 BP.
XX AC AAZ41946;
XX DT 24-JAN-2000 (first entry)
XX DE IL-12 secretion inducing CpG oligonucleotide 91.
XX KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
XX KW antigen presenting cell; infection; allergic disease.
XX OS Synthetic.
XX PN WO9951259-A2.
XX PD 14-OCT-1999.
XX PF 02-APR-1999; 99WO-US007335.
XX PR 03-APR-1998; 98US-0080729P.
XX PA (IOWA) UNIV IOWA RES FOUND.
XX PI Krieg AM, Weiner G;
XX PI PI
XX PI PI
XX DR WPI; 1999-620169/53.
XX PT Novel synergistic combinations of immunostimulatory oligonucleotides and
XX PT immunopotentiating cytokines are useful for stimulating the immune
XX PT system.
XX PS Example 8; Page 88; 91pp; English.
XX CC Sequences AAZ41856-241949 are phosphorothioate CpG oligonucleotides which
XX CC are used in the invention to induce interleukin-12 (IL-12) secretion from
XX CC human PBMC. The invention comprises stimulating an immune response in a
XX CC subject comprising administering to a subject exposed to an antigen, an
XX CC immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide
XX CC to induce a synergistic antigen specific immune response. The methods are
XX CC useful for treating cancer by stimulating an antigen specific immune
XX CC response against a cancer antigen. The methods can also be used to treat
XX CC neoplastic disorders in humans, including but not limited to: sarcoma,
XX CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
XX CC and glioma. The methods are also useful for treating infectious diseases,
XX CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
XX CC The methods may also be used to treat allergic diseases, e.g. asthma. The
XX CC methods and compositions may also be applied to treat cancer and tumours
XX CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
XX CC agricultural livestock may also be treated and include leukaemia,
XX CC haemangiopericytoma and bovine ocular neoplasia. Chronic, infectious,
XX CC contagious diseases of sheep and goats caused by the bacterium
XX CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
XX CC caused by jaagsiekte may also be treated. CpG oligonucleotides can be
XX CC useful in activating B cells, NK cells, and antigen presenting cells,
XX CC such as monocytes and macrophages. CpG oligonucleotides enhance antibody
XX CC dependent cellular cytotoxicity and can be used as an adjuvant in
XX CC conjunction with tumour antigens to protect against a tumour challenge
XX CC
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCCCTGACGTT 20
Db 1 TCCATGACGTTCCCTGACGTT 20

RESULT 5
AAZ41949
ID AAZ41949 standard; DNA; 20 BP.
XX AC AAZ41949;
XX DT 24-JAN-2000 (first entry)
XX DE IL-12 secretion inducing CpG oligonucleotide 94.
XX KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
XX KW antigen presenting cell; infection; allergic disease.
XX OS Synthetic.
XX PN WO9951259-A2.
XX PD 14-OCT-1999.
XX PF 02-APR-1999; 99WO-US007335.
XX PR 03-APR-1998; 98US-0080729P.
XX PA (IOWA) UNIV IOWA RES FOUND.
XX PI Krieg AM, Weiner G;
XX PI PI
XX PI PI
XX DR WPI; 1999-620169/53.
XX PT Novel synergistic combinations of immunostimulatory oligonucleotides and
XX PT immunopotentiating cytokines are useful for stimulating the immune
XX PT system.
XX PS Example 8; Page 89; 91pp; English.
XX CC Sequences AAZ41856-241949 are phosphorothioate CpG oligonucleotides which
XX CC are used in the invention to induce interleukin-12 (IL-12) secretion from
XX CC human PBMC. The invention comprises stimulating an immune response in a
XX CC subject comprising administering to a subject exposed to an antigen, an
XX CC immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide
XX CC to induce a synergistic antigen specific immune response. The methods are
XX CC useful for treating cancer by stimulating an antigen specific immune
XX CC response against a cancer antigen. The methods can also be used to treat
XX CC neoplastic disorders in humans, including but not limited to: sarcoma,
XX CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
XX CC and glioma. The methods are also useful for treating infectious diseases,
XX CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
XX CC The methods may also be used to treat allergic diseases, e.g. asthma. The
XX CC methods and compositions may also be applied to treat cancer and tumours
XX CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
XX CC agricultural livestock may also be treated and include leukaemia,
XX CC haemangiopericytoma and bovine ocular neoplasia. Chronic, infectious,
XX CC contagious diseases of sheep and goats caused by the bacterium
XX CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
XX CC caused by jaagsiekte may also be treated. CpG oligonucleotides can be
XX CC useful in activating B cells, NK cells, and antigen presenting cells,
XX CC such as monocytes and macrophages. CpG oligonucleotides enhance antibody
XX CC dependent cellular cytotoxicity and can be used as an adjuvant in
XX CC conjunction with tumour antigens to protect against a tumour challenge
XX CC
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCCCTGACGTT 20
Db 1 TCCATGACGTTCCCTGACGTT 20

RESULT 6
AAx78802
ID AAX78802 standard; DNA; 20 BP.
XX
AC AAX78802;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein CpG oligonucleotide 1.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW immunological fusion partner; CpG oligonucleotide; immune response;
KW HPV antigen; prevention; treatment; primer; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
XX WO9933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Gerard CMG;
XX
XX WPI; 1999-405485/34.
XX
DR Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.
PT
XX
PS Claim 11; Page 36; 62pp; English.
XX
CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours. This sequence represents a
CC CpG oligonucleotide which is used in the method of the invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
Db 1 TCCATGACGTTCTGACGTT 20
RESULT 7
AAZ31943
ID AAZ31943 standard; DNA; 20 BP.
XX
AC AAZ31943;
XX
DT 26-JAN-2000 (first entry)
XX
DE CpG adjuvant oligo 1001.
XX
KW CpG adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
KW antigen; infection; allergy; cancer; therapy; ss.
XX
OS Synthetic.
XX

PN WO9952549-A1.
XX
PD 21-OCT-1999.
XX
PF 29-MAR-1999; 99WO-EP002278.
XX
PR 09-APR-1998; 98GB-00007805.
PR 25-SEP-1998; 98GB-00020956.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Friede M, Hermand P;
XX
DR WPI; 1999-620290/53.
XX
PT Vaccine to protect against infections, allergy and cancer.
XX
XX Claim 16; Page 32; 52pp; English.
XX
CC This sequence represents a CpG adjuvant that can be used in the vaccine
CC composition of the invention. The vaccine comprises a polyoxyethylene
CC ether or ester (I), not in the form of a vesicle, pharmaceutically
CC acceptable excipient and an antigen (Ag) or antigenic composition. The
CC vaccine can be used to treat or prevent infections (by bacteria, viruses
CC or other parasites), allergy and cancer. (I), which are safe, easy to
CC sterilize and simple to administer, are powerful vaccine adjuvants, able
CC to induce a systemic immune response when administered (non-invasively)
CC to the mucosa. The response is at least as good as that from conventional
CC systemic injection. (I) are effective at low concentration, have low
CC reactogenicity and are well tolerated
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTGACGTT 20
Db 1 TCCATGACGTTCTGACGTT 20
RESULT 8
AAV74237
ID AAV74237 standard; DNA; 20 BP.
XX
AC AAV74237;
XX
XX 20-MAR-2003 (revised)
DT 15-MAR-1999 (first entry)
XX
DE CpG-N motif S-ODN 1826 DNA.
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS Synthetic.
XX
XX WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010408.
XX
PR 20-MAY-1997; 97US-0047209P.
PR 20-MAY-1997; 97US-0047233P.
XX
XX (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (IOWA) UNIV IOWA RES FOUND.
PA (QIAG-) QIAGEN GMBH.
XX

CC removing neutralising CpG (CpG-N) motifs and optionally inserting
 CC stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
 CC nucleic acid construct having enhanced immunostimulatory efficacy. The
 CC method can be used for immunisation against viral antigens, e.g. from
 CC hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
 CC parasite. They can also be used for expression of a therapeutic
 CC polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
 CC apoptotic proteins, interferons, hormones, clotting factors, ligands and
 CC receptors. (Updated on 20-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11

AAZ88536

ID AAZ88536 standard; DNA; 20 BP.

AC AAZ88536;

DT 10-SEP-1999 (first entry)

XX Cytosine-guanosine dinucleotide motif oligonucleotide #3.

XX Cytosine-guanosine dinucleotide motif; CpG; immunomodulation;
 KW unethylated; vaccine; immunostimulation; immune response;
 KW T-independent type 1 antigen; T-independent type 2 antigen;
 KW polysaccharide conjugate antigen; ss.

XX Synthetic.

XX WO9933488-A2.

PN 08-JUL-1999.

XX 18-DEC-1998; 98WO-EP008562.

XX 24-DEC-1997; 97GB-00027262.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Dalemans WLJ, Laferriere CAJ, Prieels J;

XX WPI; 1999-405369/34.

XX A vaccine composition for inducing an immune response to T-independent
 PT type 1 or type 2 antigen or polysaccharide conjugate antigen.

XX Claim 6; Page 31; 35pp; English.

XX The present invention describes a formulation (A) comprising a cytosine-
 CC guanosine dinucleotide motif (CpG) oligonucleotide and T-independent type
 CC 1 or type 2 antigen or polysaccharide conjugate antigen. The present
 CC sequence represent a specifically claimed CpG oligonucleotide. A vaccine
 CC composition comprising the formulation is used for inducing an immune
 CC response to T-independent type 1 or type 2 antigen or polysaccharide
 CC conjugate antigen. The use of immunostimulatory CpG oligonucleotide acts
 CC as an adjuvant to pneumococcal polysaccharides

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12

AAZ28191

ID AAZ28191 standard; DNA; 20 BP.

XX AAZ28191;

XX 20-DEC-1999 (first entry)

XX Chlamydia trachomatis outer membrane protein gene-derived CpG oligo 4.

XX Heart disease; inflammatory; autoimmune; cardiomyopathy; adjuvant;

KW CpG motif; vaccine; ds.

XX Synthetic.

XX Chlamydia trachomatis.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER = phosphorothioate linkage"

XX US5962636-A.

XX 05-OCT-1999.

XX 12-AUG-1998; 98US-00133774.

XX 12-AUG-1998; 98US-00133774.

XX (AMGE-) AMGEN CANADA INC.

XX Bachmaier K, Hessel AJ, Penninger JM, Neu N;

XX WPI; 1999-589735/50.

XX Peptides that induce or suppress inflammatory cardiomyopathy.

XX Example 2; Col 25; 17pp; English.

XX This sequence represents DNA encoding Chlamydia trachomatis 60 kD outer
 CC membrane protein (OMP) gene-derived CpG oligonucleotide 4. This
 CC oligonucleotide contains a CpG motif. It was tested for its ability to
 CC act as an adjuvant for the M7A-alpha peptide (AAZ42723), which can induce
 CC inflammatory cardiomyopathy (ICM) in mice. It was found to act as a
 CC potent immunostimulator, whereas a oligonucleotide from the same source
 CC which did not contain a CpG motif (AAZ28193) was hardly effective as an
 CC adjuvant. Inflammatory cardiomyopathy peptides (AAZ42723, AAZ42725-
 CC Y42731) can be used with such an adjuvant and an excipient in a vaccine
 CC for decreasing ICM

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13

AAZ61012

ID AAZ61012 standard; DNA; 20 BP.

XX AAZ61012;

XX 30-MAY-2000 (first entry)

XX DE Nucleotide sequence of an immunostimulatory CpG oligonucleotide.
 XX
 KW Immunostimulatory; stereoisomer; CpG oligonucleotide; Th2; Th1; asthma;
 KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;
 KW inflammatory disease; inflammatory bowel disease; autoimmune disease;
 KW gingivitis; psoriasis; sepsis; ss.
 XX
 OS Synthetic.
 XX
 PN WO200006588-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 27-JUL-1999; 99WO-US017100.
 XX
 PR 27-JUL-1998; 98US-0094370P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
 XX
 PI Krieg AM;
 XX
 DR WPI; 2000-195254/17.
 XX
 PT Immunostimulatory and immunoinhibitory stereoisomers of CpG
 PT oligonucleotides useful for immunotherapy of cancer.
 XX
 PS Disclosure; Page 12; 88pp; English.
 XX
 CC AAZ60933-261015 represent immunostimulatory stereoisomers of CpG
 CC oligonucleotides. The sequences are derived from generic nucleic acid
 CC sequence, from which immunoinhibitory sequences may also be derived. The
 CC immunostimulatory nucleic acids can be co-administered with an antigen to
 CC induce an antigen-specific immune response. The immunostimulatory nucleic
 CC acids can also be used in methods for redirecting a subject's immune
 CC response from a Th2 to a Th1, for treating asthma, for desensitising a
 CC subject against the occurrence of an allergic reaction in response to
 CC contact with an allergen, for activating an immune cell, especially a
 CC lymphocyte or a dendritic cell expressing a cancer antigen or for
 CC treating cancer. The immunoinhibitory nucleic acid can be used to prevent
 CC an immune response, especially where the immune response in the subject
 CC is excessive due to having received an immune stimulating compound. The
 CC immunoinhibitory nucleic acid can be used to treat a subject having or at
 CC risk of an inflammatory disease, especially inflammatory bowel disease,
 CC autoimmune disease, gingivitis, psoriasis and sepsis
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTCTGACGTT 20
 DB 1 TCCATGACGTTCTCTGACGTT 20
 RESULT 14
 AAZ61010
 ID AAZ61010 standard; DNA; 20 BP.
 XX
 AC AAZ61010;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Nucleotide sequence of an immunostimulatory CpG oligonucleotide.
 XX
 KW Immunostimulatory; stereoisomer; CpG oligonucleotide; Th2; Th1; asthma;
 KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;
 KW inflammatory disease; inflammatory bowel disease; autoimmune disease;
 KW gingivitis; psoriasis; sepsis; ss.
 XX

OS Synthetic.
 XX
 PN WO200006588-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 27-JUL-1999; 99WO-US017100.
 XX
 PR 27-JUL-1998; 98US-0094370P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
 XX
 PI Krieg AM;
 XX
 DR WPI; 2000-195254/17.
 XX
 PT Immunostimulatory and immunoinhibitory stereoisomers of CpG
 PT oligonucleotides useful for immunotherapy of cancer.
 XX
 PS Disclosure; Page 12; 88pp; English.
 XX
 CC AAZ60933-261015 represent immunostimulatory stereoisomers of CpG
 CC oligonucleotides. The sequences are derived from generic nucleic acid
 CC sequence, from which immunoinhibitory sequences may also be derived. The
 CC immunostimulatory nucleic acids can be co-administered with an antigen to
 CC induce an antigen-specific immune response. The immunostimulatory nucleic
 CC acids can also be used in methods for redirecting a subject's immune
 CC response from a Th2 to a Th1, for treating asthma, for desensitising a
 CC subject against the occurrence of an allergic reaction in response to
 CC contact with an allergen, for activating an immune cell, especially a
 CC lymphocyte or a dendritic cell expressing a cancer antigen or for
 CC treating cancer. The immunoinhibitory nucleic acid can be used to prevent
 CC an immune response, especially where the immune response in the subject
 CC is excessive due to having received an immune stimulating compound. The
 CC immunoinhibitory nucleic acid can be used to treat a subject having or at
 CC risk of an inflammatory disease, especially inflammatory bowel disease,
 CC autoimmune disease, gingivitis, psoriasis and sepsis
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTCTGACGTT 20
 DB 1 TCCATGACGTTCTCTGACGTT 20
 RESULT 15
 AAZ48025
 ID AAZ48025 standard; DNA; 20 BP.
 XX
 AC AAZ48025;
 XX
 DT 08-MAR-2000 (first entry)
 XX
 DE Immune remodeling inducing CpG oligonucleotide SEQ ID NO:105.
 XX
 KW Haematopoiesis; regulation; CpG oligonucleotide; phosphorothioate;
 KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
 KW immune response; allergic reaction; infectious disease; asthma;
 KW thrombocytopenia; immunohaemolytic disorder; genetic disorder;
 KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;
 KW rheumatoid arthritis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9558118-A2.
 XX
 PD 18-NOV-1999.
 XX

PF 14-MAY-1999; 99WO-1B001285.
XX
PR 14-MAY-1998; 98US-0085516P.
PR 02-FEB-1999; 99US-00241653.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
PI Wagner H, Lipford G;
XX
XX WPI; 2000-062261/05.
XX
XX Use of CpG containing oligonucleotides for, e.g. inducing an antigen-
PT specific immune response.
XX
PS Example 1; Page 67; 116pp; English.
XX
XX The present invention describes a method using CpG containing
CC oligonucleotides (ONs) for regulating immune system remodeling and for
CC regulating haematopoiesis. The method for inducing an antigen-specific
CC immune response comprises: (1) administering an ON having a sequence
CC including at least the formula (I); and (2) exposing the subject to an
CC antigen at least 3 days after the ON is administered to the subject to
CC produce an antigen-specific immune response: 5' X1CGX2 3' (I), where the
CC ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and
CC X2 = nucleotides. The method can be used for inducing an immune response
CC against an antigen such as cells, cell extracts, proteins,
CC polysaccharides, polysaccharide conjugates, lipids, glycolipids,
CC carbohydrates, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or an
CC allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia which
CC is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as drug
CC -induced anaemia, immunohaemolytic disorder, genetic disorders such as
CC haemoglobinopathy and inherited haemolytic anaemia, inadequate production
CC despite adequate iron stores, chronic disease such as kidney failure, and
CC chronic inflammatory disorder such as rheumatoid arthritis, or anaemia
CC resulting from accidental or therapeutic radiation exposure. AAZ47932 to
CC AAZ48029 represent phosphorothioate CpG oligonucleotides used in the
CC exemplification of the present invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGACGTT 20
|||
Db 1 TCCATGACGTTCTGACGTT 20

Search completed: May 4, 2006, 02:44:24
Job time : 150.46 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 01:23:12 ; Search time 135.414 Seconds
(without alignments)
885.910 Million cell updates/sec

Title: US-10-789-758A-2

Perfect score: 18
Sequence: 1 ttctccagcgtgcgcac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_21.1*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	2	AaQ86659 Bcl-2 ant
2	18	100.0	18	2	AaV52545 Unmethyila
3	18	100.0	18	2	AaV28181 Antisense
4	18	100.0	18	2	AaV27719 Immunosti
5	18	100.0	18	2	AaV19667 Human bcl
6	18	100.0	18	2	AaZ1948 IL-12 sec
7	18	100.0	18	2	AaZ1905 IL-12 sec
8	18	100.0	18	2	AaX78803 HPV fusio
9	18	100.0	18	2	AaV99434 Antisense
10	18	100.0	18	2	AaZ31944 Cpg adjuv
11	18	100.0	18	2	AaX27536 Synthetic
12	18	100.0	18	2	AaX18702 target bc
13	18	100.0	18	2	AaX88537 Cytosine-
14	18	100.0	18	2	AaX33514 BCL2-targ
15	18	100.0	18	2	AaX23693 Deletion
16	18	100.0	18	3	AaZ60975 Nucleotid
17	18	100.0	18	3	AaZ48024 Immune re
18	18	100.0	18	3	AaZ47981 Immune re
19	18	100.0	18	3	AaA14470 Phosphoro

20	18	100.0	18	3	AaZ87997	AaZ87997 BBTE-labe
21	18	100.0	18	3	AaZ47850	AaZ47850 Immunosti
22	18	100.0	18	3	AaA38517	AaA38517 Oligonucl
23	18	100.0	18	3	AaA90450	AaA90450 Cpg adjuv
24	18	100.0	18	3	AaZ99003	AaZ99003 Cpg motif
25	18	100.0	18	3	AaZ98660	AaZ98660 Human Bcl
26	18	100.0	18	3	AaA39264	AaA39264 Cpg immun
27	18	100.0	18	3	AaZ47680	AaZ47680 Parasitic
28	18	100.0	18	3	AaZ47643	AaZ47643 Parasitic
29	18	100.0	18	3	AaA91620	AaA91620 Human Bcl
30	18	100.0	18	3	AaC60278	AaC60278 Immunosti
31	18	100.0	18	3	AaC65037	AaC65037 Bcl2 anti
32	18	100.0	18	3	AaC64137	AaC64137 Immunosti
33	18	100.0	18	4	AaH20395	AaH20395 Cpg motif
34	18	100.0	18	4	AaH50615	AaH50615 Natural k
35	18	100.0	18	4	AaF60923	AaF60923 Anti-bcl
36	18	100.0	18	4	AaH19305	AaH19305 Cpg oligo
37	18	100.0	18	4	AaF98832	AaF98832 Cpg immun
38	18	100.0	18	4	AaF59502	AaF59502 Immunosti
39	18	100.0	18	4	AaF98930	AaF98930 Immunosti
40	18	100.0	18	4	AaF98929	AaF98929 Immunosti
41	18	100.0	18	4	AaF98966	AaF98966 Immunosti
42	18	100.0	18	4	AaF98885	AaF98885 Immunosti
43	18	100.0	18	4	AaA92362	AaA92362 CG motif
44	18	100.0	18	5	AaS08980	AaS08980 Cpg-conta
45	18	100.0	18	5	AaF27748	AaF27748 P. falcip

ALIGNMENTS

RESULT 1

AAQ86659

ID AAQ86659 standard; DNA; 18 BP.

XX AAQ86659;

XX 25-MAR-2003 (revised)

DT 27-SEP-1995 (first entry)

XX Bcl-2 antisense oligonucleotide.

XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW chemoresistance; ss.
XX Synthetic.
XX Key misc_feature Location/Qualifiers
FT 1..18
FT /*tag= a
FT /note= "3'-5' (antisense) sequence"
XX WO9508350-A1.
XX 30-MAR-1995.
XX 20-SEP-1994; 94WO-US010725.
XX 20-SEP-1993; 93US-00124256.
XX (REED/) REED J C.
XX Reed JC;
XX WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human
PT solid tumours, esp. breast cancer.
XX Example 18; Page 44; 108pp; English.
XX Reversal of chemoresistance of tumor cells by antisense-mediated
CC reduction of bcl1-2 expression was demonstrated using the oligonucleotide

CC given in AAQ86659. This is antisense to the first 6 codons of the bcl-2
 CC ORF. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACAGCGTGGCCAT 18

Db 1 TCTCCACAGCGTGGCCAT 18

RESULT 2

AAV52545

ID AAV52545 standard; DNA; 18 BP.

XX

AC AAV52545;

XX

DT 20-NOV-1998 (first entry)

XX

DE Unmethylated CpG dinucleotide 1758.

XX

KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 pulmonary disorder; asthma; environmentally induced airway disease;
 bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 inflammatory bowel disease; ss.

XX

OS Synthetic.

XX

PN WO9837919-A1.

XX

PD 03-SBP-1998.

XX

PF 25-FEB-1998; 98WO-US003678.

XX

PR 28-FEB-1997; 97US-0039405P.

XX

PA (IOWA) UNIV IOWA RES FOUND.

XX

PI Schwartz DA, Krieg AM;

XX

DR WPI; 1998-480941/41.

XX

PT Use of nucleic acids containing an unmethylated CpG - for treating a
 subject having or at risk of having an acute decrement in air flow or
 inhibiting an inflammatory response.

XX

PS Example 4; Page 35; 65pp; English.

XX

CC This sequence represents an unmethylated CpG dinucleotide, and can be
 used in the method of the invention. The method is for treating a subject
 having, or at risk of having an acute decrement in air flow, comprising
 administering a nucleic acid sequence containing at least one
 unmethylated CpG. The nucleic acid sequence containing an unmethylated CpG
 dinucleotide affect an immune response in a subject by activating natural
 killer cells (NK) or redirecting a subject's immune response from a Th2
 to a Th1 response by inducing monocytic and other cells to produce Th1
 cytokines. They can be used to treat pulmonary disorders having an
 immunologic component, such as asthma or environmentally induced airway
 disease. They can also be used to treat diseases associated with Gram-
 positive bacterial infections or endotoxaemia including bacterial
 meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 abscesses, haemorrhagic shock, disseminated intravascular coagulation, or
 an inflammatory response to lipopolysaccharide

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACAGCGTGGCCAT 18

Db 1 TCTCCACAGCGTGGCCAT 18

RESULT 3

AAV28181

ID AAV28181 standard; DNA; 18 BP.

XX

AC AAV28181;

XX

DT 08-OCT-1998 (first entry)

XX

DE Antisense oligonucleotide to bcl-2 mRNA.

XX

KW Purification; oligonucleotide; matrix; affinity unit;
 affinity purification; antisense; bcl-2; ss.

XX

OS Synthetic.

XX

PN WO9827425-A1.

XX

PD 25-JUN-1998.

XX

PF 18-DEC-1997; 97WO-US023284.

XX

PR 19-DEC-1996; 96US-00769951.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Chen D, Srivatsa GS, Cole DL;

XX

DR WPI; 1998-362922/31.

XX

PT Matrix for selective separation of oligonucleotide - useful for, e.g.
 large scale purification of anti-sense agents from their deletion
 derivatives formed during synthesis.

XX

PS Disclosure; Page 86; 183pp; English.

XX

CC AAV28155-268 represent oligonucleotides which can be purified using the
 method of the invention. The specification describes a matrix that
 comprises a support and an affinity unit that specifically and reversibly
 binds a target oligonucleotide, and comprises a sequence of bases having
 the reverse complement of a hybridising portion of the target
 oligonucleotide. The matrix is used for affinity purification of
 synthetic oligonucleotides, specifically antisense agents, for treatment
 of hyperproliferative diseases, for treating a non-pathogen, non-
 hyperproliferative disease, e.g. Alzheimer's, for modulating expression
 of cell surface proteins, and to inhibit a eukaryotic pathogen,
 retrovirus or other viruses

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACAGCGTGGCCAT 18

Db 1 TCTCCACAGCGTGGCCAT 18

RESULT 4

AAV27719

ID AAV27719 standard; DNA; 18 BP.

XX

AC AAV27719;

XX

DT 01-OCT-1998 (first entry)

XX

DE Immunostimulatory oligodeoxyribonucleotide of the invention.
 XX
 KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
 KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
 KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
 KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
 OS Synthetic.
 XX
 PN WO9818810-A1.
 XX
 PD 07-MAY-1998.
 XX
 XX 30-OCT-1997; 97WO-US019791.
 XX
 XX 30-OCT-1996; 96US-00738652.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 XX
 XX Krieg AM, Kline JN;
 XX
 XX WPI; 1998-272127/24.
 XX
 XX New immunostimulatory nucleic acid molecules - which contain at least one
 PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
 PT or autoimmune disease.
 XX
 XX Disclosure; Page 49; 109pp; English.
 XX
 XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
 CC of the invention. The ODNs contain at least one unmethylated CpG
 CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
 CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
 CC thymine, X2 is cytosine or thymine, N is any nucleotide, and N1+N2 is 0-26
 CC bases with the provision that N1 and N2 does not contain a CCG tetramer
 CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
 CC one nucleotide separates consecutive CpGs, X1 and X2 are selected from
 CC GpT, GpG, GpA, Apt and ApA, X3 and X4 are selected from Tpt or Cpt, N is
 CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
 CC does not contain a CCG tetramer or more than one CCG or CCG trimer. The
 CC ODNs activate lymphocytes in a subject and redirect a subject's immune
 CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other
 CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
 CC The ODNs can be used to treat or prevent an asthmatic disorder,
 CC autoimmune diseases, in desensitisation therapy, as an artificial
 CC adjuvant during antibody generation in a mammal such as a mouse or a
 CC human
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTCCACGCGTGGCCAT 18
 Db 1 TCTCCACGCGTGGCCAT 18
 RESULT 5
 AAV19667
 ID AAV19667 standard; DNA; 18 BP.
 XX
 AC AAV19667;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-JUN-1998 (first entry)
 XX
 XX Human bcl-2 antisense oligonucleotide 13.
 DE
 XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 KW cancer; ss.
 XX

OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 XX 24-MAR-1994; 94US-00217082.
 XX
 XX 22-DEC-1988; 88US-00288692.
 PR
 PR 21-FEB-1992; 92US-00840716.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 XX Reed J;
 XX
 XX WPI; 1998-229881/20.
 DR
 XX Anti-sense oligonucleotide(s) complementary to BCL-2 mRNA - useful for
 PT treating cancers, e.g. lymphoma(s) and some leukaemia(s).
 XX
 XX Disclosure; Col 23; 21pp; English.
 XX
 XX This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTCCACGCGTGGCCAT 18
 Db 1 TCTCCACGCGTGGCCAT 18
 RESULT 6
 AAZ41948
 ID AAZ41948 standard; DNA; 18 BP.
 XX
 AC AAZ41948;
 XX
 XX 24-JAN-2000 (first entry)
 DT
 XX IL-12 secretion inducing CpG oligonucleotide 93.
 DE
 XX CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
 KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 KW antigen presenting cell; infection; allergic disease.
 XX
 OS Synthetic.
 OS
 PN WO9951259-A2.
 XX
 XX 14-OCT-1999.
 PD
 XX 02-APR-1999; 99WO-US007335.
 PF
 XX 03-APR-1998; 98US-0080729P.
 PR
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX Krieg AM, Weiner G;
 XX

```

XX WPI; 1999-620169/53.
DR
XX
XX Novel synergistic combinations of immunostimulatory oligonucleotides and
PT immunopotentiating cytokines are useful for stimulating the immune
PT system.
XX
XX Example 8; Page 88; 91pp; English.
PS
XX
XX Sequences AAZ41856-241949 are phosphorothioate CpG oligonucleotides which
CC are used in the invention to induce interleukin-12 (IL-12) secretion from
CC human PBMC. The invention comprises stimulating an immune response in a
CC subject comprising administering to a subject exposed to an antigen, an
CC immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide
CC to induce a synergistic antigen specific immune response. The methods are
CC useful for treating cancer by stimulating an antigen specific immune
CC response against a cancer antigen. The methods can also be used to treat
CC neoplastic disorders in humans, including but not limited to: sarcoma,
CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
CC and glioma. The methods are also useful for treating infectious diseases,
CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
CC The methods may also be used to treat allergic diseases, e.g. asthma. The
CC methods and compositions may also be applied to treat cancer and tumours
CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
CC agricultural livestock may also be treated and include leukaemia,
CC haemangiopericytoma and bovine ocular neoplasia. Chronic, infectious,
CC contagious diseases of sheep and goats caused by the bacterium
CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
CC caused by jaagsiekte may also be treated. CpG oligonucleotides can be
CC useful in activating B cells, NK cells, and antigen presenting cells,
CC such as monocytes and macrophages. CpG oligonucleotides enhance antibody
CC dependent cellular cytotoxicity and can be used as an adjuvant in
CC conjunction with tumour antigens to protect against a tumour challenge
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCAGCGTGCGCCAT 18
Db 1 TCTCCAGCGTGCGCCAT 18
RESULT 7
AAZ41905
ID AAZ41905 standard; DNA; 18 BP.
XX
XX AAZ41905;
XX
XX 24-JAN-2000 (first entry)
XX
XX IL-12 secretion inducing CpG oligonucleotide 50.
XX
XX CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
XX human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
XX neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
XX antigen presenting cell; infection; allergic disease.
XX
XX Synthetic.
XX
XX WO9951259-A2.
XX
XX 14-OCT-1999.
XX
XX 02-APR-1999; 99WO-US007335.
XX
XX 03-APR-1998; 98US-0080729P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Krieg AM, Weiner G;
PI
XX WPI; 1999-620169/53.
DR
XX
XX Novel synergistic combinations of immunostimulatory oligonucleotides and
PT immunopotentiating cytokines are useful for stimulating the immune
PT system.
XX
XX Example 8; Page 80; 91pp; English.
PS
XX
XX Sequences AAZ41856-241949 are phosphorothioate CpG oligonucleotides which
CC are used in the invention to induce interleukin-12 (IL-12) secretion from
CC human PBMC. The invention comprises stimulating an immune response in a
CC subject comprising administering to a subject exposed to an antigen, an
CC immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide
CC to induce a synergistic antigen specific immune response. The methods are
CC useful for treating cancer by stimulating an antigen specific immune
CC response against a cancer antigen. The methods can also be used to treat
CC neoplastic disorders in humans, including but not limited to: sarcoma,
CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
CC and glioma. The methods are also useful for treating infectious diseases,
CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
CC The methods may also be used to treat allergic diseases, e.g. asthma. The
CC methods and compositions may also be applied to treat cancer and tumours
CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
CC agricultural livestock may also be treated and include leukaemia,
CC haemangiopericytoma and bovine ocular neoplasia. Chronic, infectious,
CC contagious diseases of sheep and goats caused by the bacterium
CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
CC caused by jaagsiekte may also be treated. CpG oligonucleotides can be
CC useful in activating B cells, NK cells, and antigen presenting cells,
CC such as monocytes and macrophages. CpG oligonucleotides enhance antibody
CC dependent cellular cytotoxicity and can be used as an adjuvant in
CC conjunction with tumour antigens to protect against a tumour challenge
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCAGCGTGCGCCAT 18
Db 1 TCTCCAGCGTGCGCCAT 18
RESULT 8
AAZ78803
ID AAX78803 standard; DNA; 18 BP.
XX
XX AAX78803;
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein CpG oligonucleotide 2.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; primer; ss.
XX
XX Synthetic.
XX
XX Human papillomavirus.
XX
XX WO9933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-BP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
PI

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XX WPI; 1999-405485/34.
 XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 PT induce immune response to HPV.
 XX
 PS Claim 11; Page 37; 62pp; English.
 XX
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory CpG
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours. This sequence represents a
 CC CpG oligonucleotide which is used in the method of the invention
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18
 RESULT 9
 AAV99434
 ID AAV99434 standard; DNA; 18 BP.
 XX
 AC AAV99434;
 XX
 DT 22-MAR-1999 (first entry)
 XX
 DE Antisense oligonucleotide directed against human bcl-2 gene.
 XX
 KW Antisense oligonucleotide; human bcl-2 gene; phosphorothioate;
 KW phosphodiester; lipid-encapsulation; tumour; aberrant gene expression;
 KW treatment; inflammation; infection; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /tag= a
 FT /note= "phosphorothioate or phosphodiester bonds"
 XX
 PN WO9851278-A2.
 XX
 PD 19-NOV-1998.
 XX
 PF 14-MAY-1998; 98WO-CA000485.
 XX
 PR 14-MAY-1997; 97US-00856374.
 XX
 PA (INEX-) INEX PHARM CORP.
 XX
 PI Semple SC, Klimuk SK, Harasym T, Hope MJ, Ansell SM, Cullis P;
 PI Scherrer P, Debeyer D;
 XX
 WPI; 1999-045179/04.
 XX
 CC Composition containing lipid-encapsulated therapeutic agent - useful,
 PT e.g. for delivering antisense molecules or ribozymes or treating diseases
 PT associated with aberrant gene expression.
 XX
 PS Disclosure; Page 23; 98pp; English.
 XX
 CC The present sequence represents an antisense oligonucleotide directed
 CC against the human bcl-2 gene. The oligonucleotide can have either

CC phosphorothioate or phosphodiester bonds. The oligonucleotide is lipid-
 CC encapsulated using the method of the invention. A composition comprising
 CC lipid-encapsulated particles of a therapeutic agent, e.g. antisense
 CC oligonucleotides, is prepared by mixing at least 2 lipids with buffered
 CC aqueous solution of charged therapeutic agent to form an intermediate
 CC mixture of lipid-encapsulated particles, and changing the pH of the
 CC mixture to neutralise at least some of the external surface charges on
 CC the particles. One lipid has a (de)protonatable group with Ka such that
 CC the lipid is charged at a first pH but neutral at a second pH
 CC (particularly near physiological pH) and the buffer maintains this lipid
 CC in the charged form (i.e. cationic when the therapeutic agent is anionic
 CC in the buffer, or vice versa). The second lipid prevents particle
 CC aggregation during formation of the lipid-therapeutic agent particles.
 CC The composition is used to introduce therapeutic agents into cells, in
 CC vivo or in vitro, particularly to treat or prevent diseases associated
 CC with aberrant gene expression in mammals, specifically tumours,
 CC inflammation or infection
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTCCAGCGTGGCCAT 18
 Db 1 TCTCCAGCGTGGCCAT 18
 RESULT 10
 AAZ31944
 ID AAZ31944 standard; DNA; 18 BP.
 XX
 AC AAZ31944;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE CpG adjuvant oligo 1002.
 XX
 KW CpG adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
 KW antigen; infection; allergy; cancer; therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9952549-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 29-MAR-1999; 99WO-EP002278.
 XX
 PR 09-APR-1998; 98GB-00007805.
 PR 25-SEP-1998; 98GB-00020956.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Friede M, Hermand P;
 XX
 WPI; 1999-620290/53.
 XX
 PT Vaccine to protect against infections, allergy and cancer.
 XX
 PS Example 9; Page 26; 52pp; English.
 CC This sequence represents a CpG adjuvant that can be used in the vaccine
 CC composition of the invention. The vaccine comprises a polyoxyethylene
 CC ether or ester (I), not in the form of a vesicle, pharmaceutically
 CC acceptable excipient and an antigen (Ag) or antigenic composition. The
 CC vaccine can be used to treat or prevent infections (by bacteria, viruses
 CC or other parasites), allergy and cancer. (I), which are safe, easy to
 CC sterilize and simple to administer, are powerful vaccine adjuvants, able
 CC to induce a systemic immune response when administered (non-invasively)
 CC to the mucosa. The response is at least as good as that from conventional
 CC systemic injection. (I) are effective at low concentration, have low

CC reactogenicity and are well tolerated

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18
 |||||

RESULT 11

AA27536/c

ID AAX27536 standard; RNA; 18 BP.

XX

AC AAX27536;

XX

DT 27-MAY-1999 (first entry)

XX

DE Synthetic RNA sequence produced by the method of the invention.

XX

KW Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;

KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.

XX

OS Synthetic.

XX

PN WO9909044-A1.

XX

PD 25-FEB-1999.

XX

PF 17-AUG-1998; 98WO-EP005215.

XX

PR 18-AUG-1997; 97CH-00001931.

XX

PA (PITS/) PITSCH S.

PA (WEIS/) WEISS P A.

PA (JENN/) JENNY L.

XX

PI Pitsch S, Weiss PA, Jenny L;

XX

DR WPI; 1999-180963/15.

XX

2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have high purity, use in machine synthesis of ribonucleic acids, enable longer oligonucleotide chain construction, and larger amounts.

PT

PS Example 7; Page 26; 38pp; English.

XX

The invention relates to silyloxymethyl protected D- or L-ribonucleosides and their phosphonates (I), and silyloxymethyl halides (II). (I) are intermediates for synthesis of RNA-oligonucleotides with predetermined nucleotide sequence, particularly by machine synthesis. The groups specified above, apart from those on silyl, are those particularly for the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide products in diagnosis, therapy, and as research tools, are well known, and are not dealt with in detail. (II) is an intermediate for (I). The silyloxymethyl halide reagent is easy to prepare, and yields are high. Introduction of the silyloxymethyl group into the ribonucleoside is simple and rapid, and the acetal bond formed does not migrate, eliminating particularly the prior art problem of 2' to 3' isomerisation. The methylenedioxy group spacer between the silyl group and nucleoside ring results in less steric hindrance than bulky direct silyloxy linkages, enabling first, a range of choices for the silyl substituents, to provide, e.g., acid or base stability; and second, higher yields in coupling. Purer products are therefore obtained than in prior art, enabling larger quantities and longer chains of oligoribonucleotides to be synthesised successfully, and in shorter times

SQ Sequence 18 BP; 4 A; 4 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18
 |||||

RESULT 12

AA218702

ID AAX18702 standard; DNA; 18 BP.

XX

AC AAX18702;

XX

DT 10-MAY-1999 (first entry)

XX

DE Target bcl-2 antisense oligonucleotide BCL-2.

XX

KW Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KW Alzheimer's disease; beta-thalassemia; malaria; viral infection; HIV;

KW inflammation; ss.

XX

OS Synthetic.

XX

PN WO9901579-A1.

XX

PD 14-JAN-1999.

XX

PF 01-JUL-1998; 98WO-US013574.

XX

PR 01-JUL-1997; 97US-00886829.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Teng C, Hardee G;

XX

DR WPI; 1999-106077/09.

XX

Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability.

PT

PS Example 2; Page 86; 115pp; English.

XX

A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAX18669 to AAX18799 and AAX18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
 |||||
 DB 1 TCTCCAGCGTGGCCAT 18
 |||||


```

RESULT 13
AA08537
ID AAX08537 standard; DNA; 18 BP.
XX
AC AAX08537;
XX
DT 10-SEP-1999 (first entry)
XX
DE Cytosine-guanosine dinucleotide motif oligonucleotide #4.
XX
KW Cytosine-guanosine dinucleotide motif; CpG; immunomodulation;
KW unmethylated; vaccine; immunostimulation; immune response;
KW T-independent type 1 antigen; T-independent type 2 antigen;
KW polysaccharide conjugate antigen; ss.
XX
OS Synthetic.
XX
PN WO9933488-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-BP008562.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMITK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Laferriere CAJ, Prieels J;
XX
DR WPI; 1999-405369/34.
XX
PT A vaccine composition for inducing an immune response to T-independent
PT type 1 or type 2 antigen or polysaccharide conjugate antigen.
XX
PS Claim 6; Page 31; 35pp; English.
XX
CC The present invention describes a formulation (A) comprising a cytosine-
CC guanosine dinucleotide motif (CpG) oligonucleotide and T-independent type
CC 1 or type 2 antigens or polysaccharide conjugate antigen. The present
CC sequence represent a specifically claimed CpG oligonucleotide. A vaccine
CC composition comprising the formulation is used for inducing an immune
CC response to T-independent type 1 or type 2 antigen or polysaccharide
CC conjugate antigen. The use of immunostimulatory CpG oligonucleotide acts
CC as an adjuvant to pneumococcal polysaccharides
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACGCGTGGCCAT 18
Db 1 TCTCCACGCGTGGCCAT 18

RESULT 14
AAX33514
ID AAX33514 standard; DNA; 18 BP.
XX
AC AAX33514;
XX
DT 07-JUL-1999 (first entry)
XX
DE BCL2-targeted antisense oligonucleotide SEQ ID NO:45.
XX
KW Combinatorial antisense library; oligonucleotide analogue; RNase;
KW ribozyme; cleavage; anchor; binding; target RNA; ss.
XX
OS Synthetic.
XX
PN WO9918238-A1.
XX

PD 15-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020361.
XX
PR 02-OCT-1997; 97US-0060673P.
PR 18-AUG-1998; 98US-00136080.
XX
PA (OASI-) OASIS BIOSCIENCES INC.
XX
PI Riley TA, Brown BD, Arnold LJ;
XX
DR WPI; 1999-264039/22.
XX
PT Oligonucleotide analog compositions capable of coupling to form antisense
PT molecules.
XX
PS Example 9; Page 45; 71pp; English.
XX
CC The present invention describes a composition comprising two
CC oligonucleotide analogues, each having a binding domain and a coupling
CC moiety, where the binding domains are capable of hybridizing to a target
CC polynucleotide and the coupling moieties are capable of coupling to each
CC other in the absence of a target molecule. The composition/compound is
CC used to cleave an RNA target. The compositions can be used to determine
CC an optimal antisense site for a given mRNA or an optimal ribozyme
CC cleavage site for a target RNA. By separating the antisense molecules
CC into two or more pieces, a comprehensive antisense library can be
CC prepared in advance, rather than synthesizing a plurality of candidate
CC antisense molecules as needed. A complete library of every possible 17-
CC mer oligonucleotide, using the four natural bases, would consist of 417
CC (or about 1.7 x 1010) molecules. By providing the antisense molecules in
CC at least two components, e.g. a library of 8-mers and a library of 9-
CC mers, assembled quickly as needed, the library size is reduced to 48 +
CC 49, or 327 650 molecules. The complexity of the library can be further
CC reduced by substituting one or more universal or degenerate bases for
CC some of the natural bases. The present sequence represents an
CC oligonucleotide, which is used in an example from the present invention
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCACGCGTGGCCAT 18
Db 1 TCTCCACGCGTGGCCAT 18

RESULT 15
AAX23693
ID AAX23693 standard; DNA; 18 BP.
XX
AC AAX23693;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 146.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US018084.
XX
PR 02-SEP-1997; 97US-00923771.

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XX PA (ISIS-) ISIS PHARM INC.
XX PI Chen D, Srivatsa GS;
XX DR WPI; 1999-205198/17.
XX PT New compositions comprising sensor arrays made up of unique probe
XX PT oligonucleotides - useful for characterizing a sample of target deletion
XX PT oligonucleotides.
XX PS Example 9; Page 152; 163pp; English.
XX CC This invention describes a novel composition comprising a number of
XX CC sensor arrays, where each array comprises a unique probe oligonucleotide,
XX CC which is the reverse complement of part of a unique target
XX CC oligonucleotide present in a mixture of target deletion sequence
XX CC oligonucleotides. The compositions form a method for characterizing a
XX CC sample of target deletion oligonucleotides which are labelled and
XX CC hybridize with the probe oligonucleotides of the sensor arrays. Such
XX CC oligonucleotides and their targets are represented in AAX3548-X23709.
XX CC Oligonucleotides characterized by the method form pharmaceutical
XX CC compositions that are useful for modulating cellular adhesion or
XX CC proliferation, and being active against a eukaryotic pathogen, a human
XX CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
XX CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
XX CC characterization of deletion sequence oligonucleotides having related,
XX CC but different nucleobase sequences, and quantification of different
XX CC species of deletion sequence ("target") oligonucleotides in a mixture.
XX CC Also, if the specificity of the oligonucleotide's nucleobase sequence for
XX CC its reverse complement is not modified, the method may be performed using
XX CC oligodeoxynucleotides
XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
   |||||
Db 1 TCTCCAGCGTGGCCAT 18

Search completed: May 4, 2006, 02:44:19
Job time : 137.414 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 42.2989 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-6

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-09-133-774-12
2	20	100.0	20	3	US-09-303-862-12
3	20	100.0	20	3	US-08-738-652-10
4	20	100.0	20	3	US-09-030-701-62
5	20	100.0	20	3	US-09-286-098-100
6	20	100.0	20	3	US-09-286-098-105
7	20	100.0	20	3	US-08-960-774-10
8	20	100.0	20	3	US-09-082-649B-51
9	20	100.0	20	3	US-09-082-649B-56
10	20	100.0	20	3	US-09-082-649B-58
11	20	100.0	20	3	US-09-325-193A-86
12	20	100.0	20	3	US-09-325-193A-90
13	20	100.0	20	3	US-09-191-170-97
14	20	100.0	20	3	US-09-690-921-1
15	20	100.0	20	3	US-09-301-829A-1
16	20	100.0	20	3	US-09-692-170C-42
17	20	100.0	20	3	US-09-337-619-10
18	20	100.0	20	3	US-10-405-231A-42
19	20	100.0	20	3	US-10-238-607-42
20	20	100.0	20	3	US-09-984-365-42
21	20	100.0	20	3	US-09-565-906-1
22	20	100.0	20	3	US-09-257-188A-2
23	20	100.0	20	3	US-09-965-101-51
24	20	100.0	20	3	US-09-965-101-56

25	20	100.0	20	3	US-09-965-101-58	Sequence 58, Appl
26	20	100.0	20	3	US-10-697-055-42	Sequence 42, Appl
27	20	100.0	20	3	US-10-651-013-14	Sequence 14, Appl
28	20	100.0	20	3	US-09-917-222B-1	Sequence 1, Appl
29	20	100.0	20	3	US-09-954-987B-83	Sequence 83, Appl
30	20	100.0	20	3	US-09-672-126B-83	Sequence 83, Appl
31	20	100.0	44	3	US-09-082-649B-12	Sequence 12, Appl
c 32	20	100.0	44	3	US-09-082-649B-13	Sequence 12, Appl
c 33	20	100.0	44	3	US-09-965-101-12	Sequence 12, Appl
c 34	20	100.0	44	3	US-09-965-101-13	Sequence 13, Appl
35	18.4	92.0	20	3	US-09-954-987B-131	Sequence 131, Appl
36	17	85.0	17	3	US-09-030-701-39	Sequence 39, Appl
37	17	85.0	17	3	US-09-286-098-70	Sequence 70, Appl
38	17	85.0	17	3	US-08-960-774-70	Sequence 70, Appl
39	17	85.0	17	3	US-09-325-193A-60	Sequence 60, Appl
40	17	85.0	17	3	US-09-191-170-64	Sequence 64, Appl
41	17	85.0	17	3	US-09-337-619-70	Sequence 70, Appl
42	17	85.0	17	3	US-09-954-987B-34	Sequence 34, Appl
43	17	85.0	17	3	US-09-672-126B-50	Sequence 50, Appl
44	16.8	84.0	20	2	US-09-133-774-11	Sequence 11, Appl
45	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-133-774-12

; Sequence 12, Application US/09133774B

; Patent No. 5962636

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart

; FILE OF INVENTION: Disease

; FILE REFERENCE: A-536

; CURRENT APPLICATION NUMBER: US/09/133,774B

; CURRENT FILING DATE: 1998-08-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia trachomatis

; FEATURE:

; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a

; OTHER INFORMATION: 60 kda cysteine rich outer membrane protein from

; OTHER INFORMATION: Chlamydia trachomatis.

US-09-133-774-12

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20

Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2

US-09-303-862-12

; Sequence 12, Application US/09303862

; Patent No. 6034230

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Heart

; FILE OF INVENTION: Disease

; FILE REFERENCE: A-536

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; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-303-862-12

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3
US-08-738-652-10
; Sequence 10, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-10

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 4
US-09-030-701-62
; Sequence 62, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28

; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-62

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
US-09-286-098-100
; Sequence 100, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-100

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 6
US-09-286-098-105
; Sequence 105, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-105

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
    |||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 7
US-08-960-774-10
; Sequence 10, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-960-774-10

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
    |||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 8
US-09-082-649B-51
; Sequence 51, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
```

```
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; OTHER INFORMATION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-51

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
    |||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 9
US-09-082-649B-56
; Sequence 56, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; OTHER INFORMATION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
US-09-082-649B-56

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20
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RESULT 10
US-09-082-649B-58
; Sequence 58, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
; OTHER INFORMATION: chimera
US-09-082-649B-58

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 11
US-09-325-193A-86
; Sequence 86, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-86

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-09-325-193A-90
; Sequence 90, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-90

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13
US-09-191-170-97
; Sequence 97, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; TITLE OF INVENTION: for Activating Dendritic Cells
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 12
US-09-325-193A-90
; Sequence 90, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-90

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 13
US-09-191-170-97
; Sequence 97, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; TITLE OF INVENTION: for Activating Dendritic Cells
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
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US-09-191-170-97

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 14

US-09-690-921-1
; Sequence 1, Application US/09690921
; Patent No. 6544518
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Gerard, Catherine
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: B45181-1
; CURRENT APPLICATION NUMBER: US/09/690,921
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/02920
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/301,829
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-690-921-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 15

US-09-301-829A-1
; Sequence 1, Application US/09301829A
; Patent No. 6558670
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: B45181
; CURRENT APPLICATION NUMBER: US/09/301,829A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: GB9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising
; OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20

Search completed: May 4, 2006, 07:23:50
Job time : 42.2989 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 42.2989 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-1

Perfect score: 20
Sequence: 1 tccatgacgttcctgacggtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	2	US-09-133-774-12
2	20	100.0	20	3	US-09-303-862-12
3	20	100.0	20	3	US-08-738-652-10
4	20	100.0	20	3	US-09-030-701-62
5	20	100.0	20	3	US-09-286-098-100
6	20	100.0	20	3	US-09-286-098-105
7	20	100.0	20	3	US-08-960-774-10
8	20	100.0	20	3	US-09-082-649B-51
9	20	100.0	20	3	US-09-082-649B-56
10	20	100.0	20	3	US-09-082-649B-58
11	20	100.0	20	3	US-09-325-193A-86
12	20	100.0	20	3	US-09-325-193A-90
13	20	100.0	20	3	US-09-191-170-97
14	20	100.0	20	3	US-09-690-921-1
15	20	100.0	20	3	US-09-301-829A-1
16	20	100.0	20	3	US-09-692-170C-42
17	20	100.0	20	3	US-09-337-619-10
18	20	100.0	20	3	US-10-405-231A-42
19	20	100.0	20	3	US-10-238-607-42
20	20	100.0	20	3	US-09-984-365-42
21	20	100.0	20	3	US-09-565-906-1
22	20	100.0	20	3	US-09-257-188A-2
23	20	100.0	20	3	US-09-965-101-51
24	20	100.0	20	3	US-09-965-101-56

25	20	100.0	20	3	US-09-965-101-58	Sequence 58, Appl
26	20	100.0	20	3	US-10-697-055-42	Sequence 42, Appl
27	20	100.0	20	3	US-10-651-013-14	Sequence 14, Appl
28	20	100.0	20	3	US-09-917-222B-1	Sequence 1, Appl
29	20	100.0	20	3	US-09-954-987B-83	Sequence 83, Appl
30	20	100.0	20	3	US-09-672-126B-83	Sequence 83, Appl
31	20	100.0	44	3	US-09-082-649B-12	Sequence 12, Appl
c 32	20	100.0	44	3	US-09-082-649B-13	Sequence 13, Appl
c 33	20	100.0	44	3	US-09-965-101-12	Sequence 12, Appl
c 34	20	100.0	44	3	US-09-965-101-13	Sequence 13, Appl
35	18.4	92.0	20	3	US-09-954-987B-131	Sequence 131, Appl
36	17	85.0	17	3	US-09-030-701-39	Sequence 39, Appl
37	17	85.0	17	3	US-09-286-098-70	Sequence 70, Appl
38	17	85.0	17	3	US-08-960-774-70	Sequence 70, Appl
39	17	85.0	17	3	US-09-325-193A-60	Sequence 60, Appl
40	17	85.0	17	3	US-09-191-170-64	Sequence 64, Appl
41	17	85.0	17	3	US-09-337-619-70	Sequence 70, Appl
42	17	85.0	17	3	US-09-954-987B-34	Sequence 34, Appl
43	17	85.0	17	3	US-09-672-126B-50	Sequence 50, Appl
44	16.8	84.0	20	2	US-09-133-774-11	Sequence 11, Appl
45	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-133-774-12
; Sequence 12, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
; FILE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kda cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-12

Query Match 100.0% Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
|||||
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2
US-09-303-862-12
; Sequence 12, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Heart
; FILE OF INVENTION: Disease
; FILE REFERENCE: A-536

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; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-303-862-12

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 3
US-08-738-652-10
; Sequence 10, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-10

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 4
US-09-030-701-62
; Sequence 62, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28

; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-62

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 5
US-09-286-098-100
; Sequence 100, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-100

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 6
US-09-286-098-105
; Sequence 105, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-105

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
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Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 7
US-08-960-774-10
; Sequence 10, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-960-774-10

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
   |||||
Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 8
US-09-082-649B-51
; Sequence 51, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
```

```
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-51

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
   |||||
Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 9
US-09-082-649B-56
; Sequence 56, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
US-09-082-649B-56

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
   |||||
Db 1 TCCATGACGTTCTCGACGTT 20
```

RESULT 10
 US-09-082-649B-58
 ; Sequence 58, Application US/09082649B
 ; Patent No. 6339068
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Heather L.
 ; APPLICANT: Krieg, Arthur M.
 ; APPLICANT: Schorr, Joachim
 ; APPLICANT: Wu, Tong
 ; TITLE OF INVENTION: Vectors and Methods for Immunization or
 ; TITLE OF INVENTION: Therapeutic Protocols
 ; FILE REFERENCE: C1039/7009
 ; CURRENT APPLICATION NUMBER: US/09/082,649B
 ; CURRENT FILING DATE: 1998-05-20
 ; PRIOR APPLICATION NUMBER: US 60/047,233
 ; PRIOR FILING DATE: 1997-05-20
 ; PRIOR APPLICATION NUMBER: US 60/047,209
 ; PRIOR FILING DATE: 1997-05-20
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 58
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
 ; OTHER INFORMATION: chimera
 US-09-082-649B-58

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
 Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 11
 US-09-325-193A-86
 ; Sequence 86, Application US/09325193A
 ; Patent No. 6406705
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Heather L.
 ; APPLICANT: Schorr, Joachim
 ; APPLICANT: Krieg, Arthur M.
 ; TITLE OF INVENTION: Use of Nucleic Acids Containing
 ; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
 ; FILE REFERENCE: C1039/7025/HCL
 ; CURRENT APPLICATION NUMBER: US/09/325,193A
 ; CURRENT FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: US 09/154,614
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: PCT/US98/04703
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: US 60/040,376
 ; PRIOR FILING DATE: 1997-03-10
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 86
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 US-09-325-193A-86

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGACGTTCTCGACGTT 20
 Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 12
 US-09-325-193A-90
 ; Sequence 90, Application US/09325193A
 ; Patent No. 6406705
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Heather L.
 ; APPLICANT: Schorr, Joachim
 ; APPLICANT: Krieg, Arthur M.
 ; TITLE OF INVENTION: Use of Nucleic Acids Containing
 ; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
 ; FILE REFERENCE: C1039/7025/HCL
 ; CURRENT APPLICATION NUMBER: US/09/325,193A
 ; CURRENT FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: US 09/154,614
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: PCT/US98/04703
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: US 60/040,376
 ; PRIOR FILING DATE: 1997-03-10
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide
 US-09-325-193A-90

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCGACGTT 20
 Db 1 TCCATGACGTTCTCGACGTT 20

RESULT 13
 US-09-191-170-97
 ; Sequence 97, Application US/09191170
 ; Patent No. 6429199
 ; GENERAL INFORMATION:
 ; APPLICANT: Krieg, Arthur M.
 ; APPLICANT: Hartmann, Gunther
 ; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
 ; TITLE OF INVENTION: for Activating Dendritic Cells
 ; FILE REFERENCE: C1039/7017
 ; CURRENT APPLICATION NUMBER: US/09/191,170
 ; CURRENT FILING DATE: 1998-11-13
 ; EARLIER APPLICATION NUMBER: US 08/960,774
 ; EARLIER FILING DATE: 1997-10-30
 ; EARLIER APPLICATION NUMBER: US 08/738,652
 ; EARLIER FILING DATE: 1996-10-30
 ; EARLIER APPLICATION NUMBER: US 08/386,063
 ; EARLIER FILING DATE: 1995-02-07
 ; EARLIER APPLICATION NUMBER: US 08/276,358
 ; EARLIER FILING DATE: 1994-07-15
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 97
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic oligonucleotide

US-09-191-170-97

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

QY 1 TCCATGACGTTCTCTGACGTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCATGACGTTCTCTGACGTT 20

Search completed: May 4, 2006, 07:23:50
Job time : 42.2989 secs

RESULT 14

US-09-690-921-1
; Sequence 1, Application US/09690921
; Patent No. 6544518
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Gerard, Catherine
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: B45181-1
; CURRENT APPLICATION NUMBER: US/09/690,921
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/02920
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/301,829
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-690-921-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCTGACGTT 20
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Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 15

US-09-301-829A-1
; Sequence 1, Application US/09301829A
; Patent No. 6558670
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: B45181
; CURRENT APPLICATION NUMBER: US/09/301,829A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: GB9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising
; OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 38.069 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-2

Perfect score: 18
Sequence: 1 tctccagctgctgcacat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/prodata/1/ina/5_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/H_COMB.seq:*
6: /cgn2_6/prodata/1/ina/ECTUS_COMB.seq:*
7: /cgn2_6/prodata/1/ina/FP_COMB.seq:*
8: /cgn2_6/prodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	2	US-08-217-082A-17
2	18	100.0	18	2	US-08-465-485A-17
3	18	100.0	18	2	US-08-465-485A-24
4	18	100.0	18	3	US-09-080-285-17
5	18	100.0	18	3	US-09-080-285-24
6	18	100.0	18	3	US-09-249-730-218
7	18	100.0	18	3	US-09-118-220-1
8	18	100.0	18	3	US-08-738-652-55
9	18	100.0	18	3	US-09-030-701-27
10	18	100.0	18	3	US-09-286-098-59
11	18	100.0	18	3	US-09-286-098-104
12	18	100.0	18	3	US-08-960-774-45
13	18	100.0	18	3	US-09-078-954-14
14	18	100.0	18	3	US-09-325-193A-51
15	18	100.0	18	3	US-09-724-426-17
16	18	100.0	18	3	US-09-724-426-24
17	18	100.0	18	3	US-09-191-170-53
18	18	100.0	18	3	US-09-136-080E-45
19	18	100.0	18	3	US-09-690-921-2
20	18	100.0	18	3	US-09-301-829A-2
21	18	100.0	18	3	US-09-249-247-218
22	18	100.0	18	3	US-09-337-619-45
23	18	100.0	18	3	US-09-835-370-21
24	18	100.0	18	3	US-09-634-320-7

c

RESULT 1

US-08-217-082A-17
; Sequence 17, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA

ALIGNMENTS

25	18	100.0	18	3	US-09-654-373-14	Sequence 14, Appl
26	18	100.0	18	3	US-09-724-425-17	Sequence 17, Appl
27	18	100.0	18	3	US-09-724-425-24	Sequence 24, Appl
28	18	100.0	18	3	US-09-895-480A-14	Sequence 14, Appl
29	18	100.0	18	3	US-10-002-884A-6	Sequence 6, Appl
30	18	100.0	18	3	US-09-108-673A-34	Sequence 34, Appl
31	18	100.0	18	3	US-09-835-371-21	Sequence 21, Appl
32	18	100.0	18	3	US-09-954-987B-115	Sequence 115, App
33	18	100.0	18	3	US-09-672-126B-110	Sequence 110, App
34	18	100.0	19	3	US-09-634-320-8	Sequence 8, Appl
35	18	100.0	19	3	US-09-634-320-9	Sequence 9, Appl
36	18	100.0	20	3	US-09-082-649B-60	Sequence 60, Appl
37	18	100.0	20	3	US-09-965-101-60	Sequence 60, Appl
38	18	100.0	23	3	US-09-634-320-1	Sequence 1, Appl
39	18	100.0	23	3	US-09-634-320-2	Sequence 2, Appl
40	18	100.0	27	2	US-08-410-804-13	Sequence 13, Appl
41	18	100.0	27	2	US-08-607-269-8	Sequence 8, Appl
42	18	100.0	27	2	US-08-259-514-13	Sequence 13, Appl
43	18	100.0	27	2	US-08-858-311-13	Sequence 13, Appl
44	18	100.0	27	6	PCT-US95-04600-8	Sequence 8, Appl
45	18	100.0	33	3	US-09-249-585A-11	Sequence 11, Appl

US-08-217-082A-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
Db 1 TCTCCAGCGTGGCCAT 18

RESULT 2

US-08-465-485A-17
; Sequence 17, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION/DOCKET NUMBER: 3335-070-55 CONT

TELEPHONE: (408) 436-2075
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-465-485A-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
Db 1 TCTCCAGCGTGGCCAT 18

RESULT 3

US-08-465-485A-24
; Sequence 24, Application US/08465485A
; Patent No. 5831066

; GENERAL INFORMATION:

; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.
REGISTRATION/DOCKET NUMBER: 3335-070-55 CONT

TELEPHONE: (408) 436-2075
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
FEATURE:

NAME/KEY: Modified_base
LOCATION: 16..17

OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates

US-08-465-485A-24

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
Db 1 TCTCCAGCGTGGCCAT 18

RESULT 4

US-09-080-285-17
; Sequence 17, Application US/09080285
; Patent No. 6040181

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION/DOCKET NUMBER: 3335-070-55 CONT

TELEPHONE: (408) 436-2075

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-465-485A-17

STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-080-285-17

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 5

US-09-080-285-24

Sequence 24, Application US/09080285

Patent No. 6040181

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-09-080-285-24

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 6

US-09-249-730-218

Sequence 218, Application US/09249730

Patent No. 6121000

GENERAL INFORMATION:

APPLICANT: WRIGHT, Jim A.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and

FILE REFERENCE: 032396-040

CURRENT APPLICATION NUMBER: US/09/249,730

CURRENT FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 220

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 218

LENGTH: 18

TYPE: DNA

ORGANISM: Human

US-09-249-730-218

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18

Db 1 TCTCCAGCGTGGCCAT 18

RESULT 7
US-09-118-220-1
; Sequence 1, Application US/09118220
; Patent No. 6140051
; GENERAL INFORMATION:
; APPLICANT: Brown, Lauren R.
; APPLICANT: Xu, Cheng
; TITLE OF INVENTION: FLUORESCENT DIBENZAZOLE DERIVATIVES
; TITLE OF INVENTION: AND METHODS RELATED THERETO
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/118,220
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfield, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/DOCKET NUMBER: GENTA.050A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-118-220-1
Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCACAGCGTGGCCAT 18
Db 1 TCTCCACAGCGTGGCCAT 18
RESULT 8
US-08-738-652-55
; Sequence 55, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-55
Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCACAGCGTGGCCAT 18
Db 1 TCTCCACAGCGTGGCCAT 18
RESULT 9
US-09-030-701-27
; Sequence 27, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27
Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCACAGCGTGGCCAT 18
Db 1 TCTCCACAGCGTGGCCAT 18
RESULT 10
US-09-286-098-59
; Sequence 59, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Synthetic Sequence
US-09-286-098-59

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
|||||
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 11

US-09-286-098-104
Sequence 104, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE OF INVENTION: Cytokines
FILE REFERENCE: C1039/7026/HCL
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US/09/286,098
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 104
LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Sequence

US-09-286-098-104

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
|||||
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 12

US-08-960-774-45
Sequence 45, Application US/08960774
Patent No. 6239116
GENERAL INFORMATION:

APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/960,774

FILING DATE: 30-October-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652

FILING DATE: October 30, 1996

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-960-774-45

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
|||||

DB 1 TCTCCAGCGTGGCCAT 18

RESULT 13

US-09-078-954-14

Sequence 14, Application US/09078954

Patent No. 6287591

GENERAL INFORMATION:

APPLICANT: SEMPLE, Sean C.

APPLICANT: Klimuk, Sandra K.

APPLICANT: Harasym, Troy

APPLICANT: Hope, Michael J.

APPLICANT: Ansell, Steven M.

APPLICANT: Cullis, Pieter

APPLICANT: Scherrer, Peter

APPLICANT: Geiser, Timothy

APPLICANT: Zon, Gerald

APPLICANT: Debever, Dan

TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in

TITLE OF INVENTION: Lipid Vesicles

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedahl & Larson

STREET: PO Box 5270

CITY: Frisco

STATE: CO

COUNTRY: USA

ZIP: 80443-5270

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS 5.0

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/078,954

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/856,374

FILING DATE: 14-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: INEX.P-003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (970) 668-2050

TELEFAX: (970) 668-2082

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

;
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
US-09-078-954-14

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
| | | | | | | | | | | | | | | | | |
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 14
US-09-325-193A-51
; Sequence 51, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-51

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
| | | | | | | | | | | | | | | | | |
DB 1 TCTCCAGCGTGGCCAT 18

RESULT 15
US-09-724-426-17
; Sequence 17, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-17

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCAGCGTGGCCAT 18
| | | | | | | | | | | | | | | | | |
DB 1 TCTCCAGCGTGGCCAT 18

Search completed: May 4, 2006, 07:23:50
Job time : 39.069 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 03:52:26 ; Search time 42.2989 Seconds
(without alignments)
840.478 Million cell updates/sec

Title: US-10-789-758A-4

Perfect score: 20
Sequence: 1 999gtcaacgttg999999 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-08-738-652-12
2	20	100.0	20	3	US-09-030-701-63
3	20	100.0	20	3	US-08-960-774-90
4	20	100.0	20	3	US-09-082-649B-52
5	20	100.0	20	3	US-09-082-649B-59
6	20	100.0	20	3	US-09-191-170-47
7	20	100.0	20	3	US-09-337-619-12
8	20	100.0	20	3	US-09-965-101-52
9	20	100.0	20	3	US-09-965-101-59
10	20	100.0	20	3	US-09-672-126B-1
11	20	100.0	20	3	US-09-672-126B-135
12	20	100.0	21	3	US-09-672-126B-156
13	18.4	92.0	20	3	US-08-386-063-1
14	18.4	92.0	20	3	US-08-386-063-1
15	17.4	87.0	19	3	US-09-030-701-21
16	17.4	87.0	19	3	US-09-286-098-52
17	17.4	87.0	19	3	US-08-960-774-12
18	17.4	87.0	19	3	US-09-325-193A-46
19	17.4	87.0	19	3	US-09-954-987B-61
20	17.4	87.0	19	3	US-09-672-126B-68
21	16.8	84.0	20	3	US-09-786-532-2
22	16.8	84.0	20	3	US-09-672-126B-5
23	16.8	84.0	20	3	US-09-672-126B-6
24	16.8	84.0	20	3	US-09-672-126B-24

25	16.8	84.0	20	3	US-09-672-126B-136	Sequence 136, App	
26	16.8	84.0	20	3	US-09-672-126B-151	Sequence 151, App	
27	16.8	84.0	21	3	US-09-672-126B-17	Sequence 17, Appl	
28	16.8	84.0	21	3	US-09-672-126B-148	Sequence 148, App	
29	16.8	84.0	84587	3	US-09-949-016-15733	Sequence 15733, A	
30	16	80.0	1426	3	US-09-464-535-41	Sequence 41, Appl	
31	15.8	79.0	19	3	US-09-672-126B-27	Sequence 27, Appl	
C	32	15.8	1674	3	US-09-482-273-78	Sequence 78, Appl	
33	15.8	79.0	2004	3	US-10-104-047-1222	Sequence 1222, Ap	
34	15.8	79.0	2312	3	US-09-620-312D-921	Sequence 921, App	
C	35	15.8	79.0	2312	3	US-09-620-312D-921	Sequence 921, App
36	15.2	76.0	20	3	US-08-386-063-27	Sequence 27, Appl	
37	15.2	76.0	20	3	US-08-386-063-27	Sequence 27, Appl	
38	15.2	76.0	30	3	US-09-672-126B-165	Sequence 165, App	
C	39	15.2	76.0	379	3	US-09-270-767-2945	Sequence 2945, Ap
C	40	15.2	76.0	379	3	US-09-270-767-18227	Sequence 18227, A
C	41	15.2	76.0	409	3	US-09-513-999C-15817	Sequence 15817, A
C	42	15.2	76.0	462	3	US-09-902-540-4875	Sequence 4875, Ap
C	43	15.2	76.0	504	3	US-09-470-191-18	Sequence 18, Appl
C	44	15.2	76.0	601	3	US-09-949-016-174326	Sequence 174326,
C	45	15.2	76.0	601	3	US-09-949-016-174518	Sequence 174518,

ALIGNMENTS

RESULT 1

US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 2

US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405

; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-63

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 3
US-08-960-774-90
; Sequence 90, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-960-774-90

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 4
US-09-082-649B-52
; Sequence 52, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-52

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
|||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 5
US-09-082-649B-59
; Sequence 59, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
; OTHER INFORMATION: in between.
US-09-082-649B-59

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 6

US-09-191-170-47
; Sequence 47, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; TITLE OF INVENTION: for Activating Dendritic Cells
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-47

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 7

US-09-337-619-12
; Sequence 12, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; TITLE OF INVENTION: Immunostimulatory Oligonucleotides
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 8

US-09-965-101-52
; Sequence 52, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; EARLIER APPLICATION NUMBER: US 09/082,649
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 60/047,233
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 60/047,209
; EARLIER FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-965-101-52

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 9

US-09-965-101-59
; Sequence 59, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; EARLIER APPLICATION NUMBER: US 09/082,649
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 60/047,233
; EARLIER FILING DATE: 1997-05-20

```

; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
; OTHER INFORMATION: in between.
US-09-965-101-59

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGTCAACGTTGAGGGGG 20
        |||||||
Db      1 GGGGTCAACGTTGAGGGGG 20

RESULT 10
US-09-672-126B-1
; Sequence 1, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)...(14)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(19)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)...(20)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-1

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGTCAACGTTGAGGGGG 20
        |||||||

```



```
; NAME/KEY: misc_feature
; LOCATION: (21)...(21)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-156

Query Match      100.0%; Score 20; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 2 GGGGTCAACGTTGAGGGGG 21

RESULT 13
US-08-386-063-1
; Sequence 1, Application US/08386063
; Patent No. 6008200
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,063
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ARNOLD, BETH E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIZ-013CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-386-063-1

Query Match      92.0%; Score 18.4; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 20
    |||||
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 15
US-09-030-701-21
; Sequence 21, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-21

Query Match      87.0%; Score 17.4; DB 3; Length 19;
Best Local Similarity 94.7%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTGAGGGGG 19
    |||||
Db 1 GGGGTCAACGTTGAGGGGG 19

RESULT 14
US-08-386-063-1
; Sequence 1, Application US/08386063
; Patent No. 6194388
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
```

Search completed: May 4, 2006, 07:23:51
Job time : 43.2989 secs